STIC Search Report
Biotech-Chem Library

USPTO

TO: Juliet Switzer
Location: REM-2A61/2C70
Art Unit: 1634
Friday, August 18, 2006
Case Serial Number: 10/600642

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

Juliet,

For the S/L search :

no suitable hits in EST for either sequence

Seg 1 / Seg 2

on disc {

N-Geneseq = ngs1.res , ngs2.res

Issued-Patents. NA iss1.res iss2.res

Genbank/EMBL ge1.res ge2.res

Published-Applications- pubmain1.res pubmain2.res
NA. Main

Published-Applications- pubnew1.res pubnew2.res
NA. New

}

Also included are the results tables for the standard searches of Segs 1, 2, 5, 6, & 10.

Barb

sira
Search and Information
Resources Administration

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.9

Run on: August 17, 2006, 05:39:06 ; Search time 217.292 Seconds
(without alignments)
5591.547 Million cell updates/sec

Title: US-10-600-642A-5
Perfect score: 19
Sequence: 1 ccatcctcttgaaaatctc 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 636136 seqs, 3193710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

(handwritten annotation: "non pat")

c	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	2	E54415	E54415 Specific an
	2	19	100.0	19	2	AR408842	AR408842 Sequence
	3	19	100.0	442	2	E54412	E54412 Specific an
c	4	19	100.0	442	2	AR408839	AR408839 Sequence
c	5	19	100.0	442	15	AB022064	AB022064 Pectinatu
	6	19	100.0	624	2	E54411	E54411 Specific an
c	7	19	100.0	624	2	AR408838	AR408838 Sequence
c	8	19	100.0	624	15	AB022063	AB022063 Pectinatu
	9	18	94.7	110000	15	AE016879_25	Continuation (26 o
c	10	18	94.7	110000	15	AE016879_26	Continuation (27 o
c	11	18	94.7	110000	15	AE017225_26	Continuation (27 o
c	12	18	94.7	110000	15	AE017334_25	Continuation (26 o
c	13	18	94.7	110000	15	AE017334_26	Continuation (27 o
c	14	18	94.7	110000	15	AE017355_26	Continuation (27 o
c	15	18	94.7	110000	15	CP000001_26	Continuation (27 o
c	16	17.4	91.6	1297	2	CQ979403	CQ979403 Sequence
c	17	17.4	91.6	1371	2	CQ979407	CQ979407 Sequence
c	18	17.4	91.6	2520	4	AB012628	AB012628 Adiantum
c	19	17.4	91.6	4557	4	AB012631	AB012631 Adiantum
c	20	17.4	91.6	68480	5	AC026426	AC026426 Homo sapi
	21	17.4	91.6	110000	4	AP008214_126	Continuation (127
c	22	17.4	91.6	146969	5	AC092945	AC092945 Homo sapi
	23	17.4	91.6	152702	4	AP005162	AP005162 Homo sapi
c	24	17.4	91.6	161353	12	AC174462	AC174462 Bos tauru
c	25	17.4	91.6	178320	4	AY360391	AY360391 Oryza sat
	26	17.4	91.6	184235	4	AP005166	AP005166 Oryza sat
c	27	17.4	91.6	186747	6	AC155266	AC155266 Mus muscu
	28	17.4	91.6	187972	4	AY360390	AY360390 Oryza sat
c	29	17.4	91.6	195998	12	AC128308	AC128308 Rattus no
	30	17.4	91.6	220797	12	AC153718	AC153718 Bos tauru
	31	17.4	91.6	227769	12	AC112437	AC112437 Rattus no
	32	17.4	91.6	232415	12	AC099429	AC099429 Rattus no
	33	17.4	91.6	245663	12	AC096102	AC096102 Rattus no
c	34	17.4	91.6	246011	6	AL929585	AL929585 Mouse DNA
c	35	17.4	91.6	252991	12	AC172968	AC172968 Bos tauru
c	36	17	89.5	563	2	CQ476058	CQ476058 Sequence
c	37	17	89.5	563	2	CQ506009	CQ506009 Sequence
c	38	17	89.5	581	7	BV268474	BV268474 S235P6405
	39	17	89.5	2027	2	CQ493216	CQ493216 Sequence
	40	17	89.5	4221	2	BD171173	BD171173 Novel gen
	41	17	89.5	4221	2	BD183502	BD183502 Novel gen
	42	17	89.5	4221	2	AB051524	AB051524 Homo sapi
	43	17	89.5	4258	5	AK096603	AK096603 Homo sapi
	44	17	89.5	4341	5	BC037300	BC037300 Homo sapi
	45	17	89.5	63987	12	AC080154	AC080154 Homo sapi

ALIGNMENTS

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:   August 17, 2006, 05:30:09 ; Search time 27.4613 Seconds
                                       (without alignments)
                            4823.973 Million cell updates/sec

Title:          US-10-600-642A-5
Perfect score:  19
Sequence:       1 ccatccctgaaaatcctc 19

Scoring table:  IDENTITY_NUC
                Gapop 10.0, Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:        10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      N_Geneseq_8:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
                14: geneseqn2005s:*
                15: geneseqn2006s:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.		Score	Query Match %	Length	DB	ID	Description
1		19	100.0	19	3	AAZ91775	Aaz91775 Spacer re
2		19	100.0	19	4	AAI71859	Aai71859 Pectinatu
3		19	100.0	19	14	ADW11499	Adw11499 PCR prime
4	c	19	100.0	442	3	AAZ91772	Aaz91772 Spacer re
5	c	19	100.0	442	4	AAI71856	Aai71856 Pectinatu
6		19	100.0	624	3	AAZ91771	Aaz91771 Spacer re
7		19	100.0	624	4	AAI71855	Aai71855 Pectinatu
8	c	17.4	91.6	1297	14	ADW38752	Adw38752 Fatty aci
9	c	17.4	91.6	1371	14	ADW38756	Adw38756 Fatty aci
10	c	17.4	91.6	46675	11	ACN44684	Acn44684 Mouse gen
11	c	17	89.5	485	4	AAL02322	Aal02322 Human rep
12		17	89.5	485	4	ABA07627	Aba07627 Human ova
13	c	17	89.5	509	5	ABV07934	Abv07934 Human pro
14	c	17	89.5	563	5	ABV37857	Abv37857 Human pro
15		17	89.5	1607	5	ABA21307	Aba21307 Human ner
16		17	89.5	2000	11	ACL38212	Acl38212 Rice stre
17		17	89.5	2000	12	ADJ41083	Adj41083 Plant cDN
18		17	89.5	2027	5	ABV25094	Abv25094 Human pro
19		17	89.5	3101	10	ADC30468	Adc30468 Human nov
20		17	89.5	3861	5	ABA21308	Aba21308 Human ner
21		17	89.5	4221	6	ABN83982	Abn83982 Human gen
22		16.4	86.3	479	11	ADT96902	Adt96902 Colon can
23		16.4	86.3	479	11	ADX43384	Adx43384 Human cDN
24		16.4	86.3	766	6	ABN99167	Abn99167 Arabidops
25		16.4	86.3	1696	6	ABZ70806	Abz70806 Human rib
26	c	16.4	86.3	5175	13	ADS17665	Ads17665 Human pol
27	c	16.4	86.3	5211	13	ADS17714	Ads17714 Cysteine
28	c	16.4	86.3	5463	13	ADS17718	Ads17718 GAL4 pept
29	c	16.4	86.3	5489	14	ADW92027	Adw92027 DNA seque
30	c	16.4	86.3	5490	4	AAZ45690	Aaz45690 cDNA sequ
31	c	16.4	86.3	5490	4	AAC92076	Aac92076 Human min
32	c	16.4	86.3	5490	10	ADB46005	Adb46005 Human min
33	c	16.4	86.3	5490	14	ADW86203	Adw86203 Human VPA
34	c	16.4	86.3	5565	13	ADS17726	Ads17726 MS2 pepti
35	c	16.4	86.3	5889	13	ADS17722	Ads17722 Green flu
36	c	16.4	86.3	6825	13	ADS17732	Ads17732 Luciferas
37	c	16.4	86.3	7302	5	AAS87290	Aas87290 DNA encod
38	c	16.4	86.3	32183	4	AAI99267	Aai99267 Human exc
39	c	16.4	86.3	32183	4	AAI63617	Aai63617 Human kid
40	c	16.4	86.3	32192	4	AAI99266	Aai99266 Human exc
41	c	16.4	86.3	32192	5	AAI63616	Aai63616 Human kid
42	c	16	84.2	1470	5	AAS75618	Aas75618 DNA encod
43	c	16	84.2	2212	4	AAK52374	Aak52374 Human pol
44	c	16	84.2	2226	4	AAC85790	Aac85790 hMfnl cDN
45	c	16	84.2	2226	8	ABX96871	Abx96871 DNA encod

ALIGNMENTS

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:     August 17, 2006, 05:57:34 ; Search time 8.03911 Seconds
                                         (without alignments)
                                    4422.263 Million cell updates/sec

Title:          US-10-600-642A-5
Perfect score:  19
Sequence:       1 ccatcctcctgaaaatcctc 19

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters:        2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
             1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
             2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
             3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
             4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
             5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
             6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
             7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
             8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
             9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
            10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfilesl.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
```

Result No.		Score	% Query Match	Length	DB	ID	Description
1	c	19	100.0	19	3	US-09-762-633-5	Sequence 5, Appli
2	c	19	100.0	442	3	US-09-762-633-2	Sequence 2, Appli
3	c	19	100.0	624	3	US-09-762-633-1	Sequence 1, Appli
4	c	16.4	86.3	5490	3	US-09-607-510-1	Sequence 1, Appli
5	c	16	84.2	2226	3	US-10-117-846-5	Sequence 5, Appli
6	c	16	84.2	2754	5	US-10-470-554-1	Sequence 1, Appli
7	c	16	84.2	2754	5	US-10-470-554-3	Sequence 3, Appli
8	c	16	84.2	3148	3	US-10-117-846-7	Sequence 7, Appli
9	c	15.8	83.2	305	3	US-09-513-999C-2094	Sequence 2094, Ap
10	c	15.8	83.2	638	3	US-09-533-559-6274	Sequence 6274, Ap
11	c	15.8	83.2	2289	3	US-08-948-705-8	Sequence 8, Appli
12	c	15.8	83.2	2289	3	US-09-510-543-8	Sequence 8, Appli
13	c	15.8	83.2	2289	4	US-09-502-945-8	Sequence 8, Appli
14	c	15.8	83.2	2409	3	US-09-510-543-9	Sequence 9, Appli
15		15.8	83.2	41743	3	US-09-949-016-13796	Sequence 13796, A
16	c	15.4	81.1	213	3	US-09-583-110-107	Sequence 107, App
17		15.4	81.1	540	3	US-09-248-796A-12682	Sequence 12682, A
18		15.4	81.1	5558	3	US-08-961-527-103	Sequence 103, App
19		15.4	81.1	9511	2	US-07-925-695-6	Sequence 6, Appli
20		15.4	81.1	9511	2	US-07-925-695-7	Sequence 7, Appli
21		15.4	81.1	45716	3	US-08-965-048-5	Sequence 5, Appli
22		15.4	81.1	45989	3	US-08-965-048-6	Sequence 6, Appli
23		15.4	81.1	72600	4	US-09-531-120-206	Sequence 206, App

24	c	15.4	81.1	283538	3	US-09-949-016-13506	Sequence 13506, A
25	c	15	78.9	6676	3	US-09-949-016-16533	Sequence 16533, A
26		15	78.9	13906	3	US-09-949-016-14730	Sequence 14730, A
27	c	14.8	77.9	32	3	US-09-826-509-400	Sequence 400, App
28		14.8	77.9	32	3	US-09-826-509-401	Sequence 401, App
29	c	14.8	77.9	107	3	US-09-959-716-23	Sequence 23, Appl
30	c	14.8	77.9	255	3	US-09-134-000C-511	Sequence 511, App
31		14.8	77.9	304	3	US-09-389-681-301	Sequence 301, App
32		14.8	77.9	304	3	US-09-620-405B-301	Sequence 301, App
33		14.8	77.9	304	3	US-09-339-338-301	Sequence 301, App
34		14.8	77.9	304	3	US-09-433-826B-301	Sequence 301, App
35		14.8	77.9	304	3	US-09-604-287A-301	Sequence 301, App
36		14.8	77.9	304	3	US-09-834-759-301	Sequence 301, App
37		14.8	77.9	304	3	US-09-590-751A-301	Sequence 301, App
38		14.8	77.9	304	3	US-09-551-621-301	Sequence 301, App
39		14.8	77.9	304	3	US-09-551-621A-301	Sequence 301, App
40		14.8	77.9	304	3	US-10-076-622-301	Sequence 301, App
41		14.8	77.9	304	4	US-10-124-805-301	Sequence 301, App
42	c	14.8	77.9	347	3	US-08-956-171E-1159	Sequence 1159, Ap
43	c	14.8	77.9	347	3	US-08-781-986A-1159	Sequence 1159, Ap
44	c	14.8	77.9	367	3	US-09-621-976-1116	Sequence 1116, Ap
45	c	14.8	77.9	413	3	US-09-513-999C-4023	Sequence 4023, Ap

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                            ALIGNMENTS
```

OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.9
           Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: August 17, 2006, 06:08:00 ; Search time 95.3716 Seconds
                                        (without alignments)
                                        2447.953 Million cell updates/sec

Title: US-10-600-642A-5
Perfect score: 19
Sequence: 1 ccatcctcctgaaaatctc 19
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 18892170 seqs, 614381763S residues
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA Main:*
    1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
    2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
    3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
    4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
    5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
    6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09D_PUBCOMB.seq:*
    7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
    8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
    9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
   10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
   11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
   12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
   13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
   14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
   15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
   16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
         /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	19	8	US-10-600-642-5	Sequence 5, Appli
2	19	100.0	442	8	US-10-600-642-2	Sequence 2, Appli
3	19	100.0	624	8	US-10-600-642-1	Sequence 1, Appli
c 4	17.4	91.6	578	4	US-09-925-065A-503267	Sequence 503267,
c 5	17.4	91.6	578	4	US-09-925-065A-503268	Sequence 503268,
c 6	17.4	91.6	578	5	US-09-925-065A-503269	Sequence 503269,
c 7	17.4	91.6	578	5	US-09-925-065A-503267	Sequence 503267,
c 8	17.4	91.6	578	5	US-09-925-065A-503268	Sequence 503268,
c 9	17.4	91.6	578	5	US-09-925-065A-503269	Sequence 503269,
c 10	17.4	91.6	1297	9	US-10-862-063A-20	Sequence 20, Appl
c 11	17.4	91.6	1371	9	US-10-862-063A-24	Sequence 24, Appl
c 12	17.4	91.6	3750	8	US-10-437-963-50726	Sequence 50726, A
c 13	17.4	91.6	4734	8	US-10-437-963-50775	Sequence 50775, A
c 14	17.4	91.6	46675	6	US-10-087-192-1255	Sequence 1255, Ap
15	17.4	89.5	485	3	US-09-764-891-2323	Sequence 2323, Ap
16	17	89.5	485	6	US-10-205-428-184	Sequence 184, App
c 17	17	89.5	509	9	US-10-357-930-7925	Sequence 7925, Ap
c 18	17	89.5	563	9	US-10-357-930-37876	Sequence 37876, A
19	17	89.5	2000	8	US-10-260-238-2083	Sequence 2083, Ap
20	17	89.5	2027	9	US-10-357-930-25083	Sequence 25083, A
c 21	17	89.5	2253	8	US-10-437-963-56352	Sequence 56352, A
c 22	16.4	86.3	467	16	US-11-087-099-174	Sequence 174, App
23	16.4	86.3	479	6	US-10-066-543-2421	Sequence 2421, Ap
24	16.4	86.3	636	4	US-09-925-065A-471436	Sequence 471436,
c 25	16.4	86.3	636	5	US-09-925-065A-471436	Sequence 471436,
c 26	16.4	86.3	661	4	US-09-925-065A-874526	Sequence 874526,
27	16.4	86.3	661	5	US-09-925-065A-874526	Sequence 874526,
28	16.4	86.3	766	5	US-09-770-445-935	Sequence 935, App
c 29	16.4	86.3	2871	8	US-10-437-963-27977	Sequence 27977, A
c 30	16.4	86.3	4547	8	US-10-437-963-50702	Sequence 50702, A
c 31	16.4	86.3	4710	8	US-10-437-963-50734	Sequence 50734, A
c 32	16.4	86.3	5490	6	US-10-163-587A-16	Sequence 16, Appl
33	16.4	86.3	5490	10	US-10-898-653-6	Sequence 6, Appli
c 34	16.4	86.3	7302	10	US-10-450-763-23094	Sequence 23094, A
c 35	16.4	86.3	32183	7	US-10-242-355-1031	Sequence 1031, Ap
c 36	16.4	86.3	32192	7	US-10-242-355-1030	Sequence 1030, Ap
c 37	16.4	86.3	87384	9	US-10-719-993-6781	Sequence 6781, Ap
38	16	84.2	50	16	US-11-175-859-70793	Sequence 70793, A
39	16	84.2	508	4	US-09-925-065A-789633	Sequence 789633,
c 40	16	84.2	508	5	US-09-925-065A-789633	Sequence 789633,
c 41	16	84.2	1470	10	US-10-450-763-11422	Sequence 11422, A
42	16	84.2	2226	6	US-10-117-846-5	Sequence 5, Appli
c 43	16	84.2	2340	8	US-10-276-774-955	Sequence 955, App
c 44	16	84.2	2754	8	US-10-470-554-1	Sequence 1, Appli
c 45	16	84.2	2754	8	US-10-470-554-3	Sequence 3, Appli

ALIGNMENTS

```
            GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:     August 17, 2006, 06:09:34 ; Search time 10.2347 Seconds
                                         (without alignments)
                                 2967.635 Million cell updates/sec

Title:            US-10-600-642A-5
Perfect score:    19
Sequence:         1 ccatcctcctgaaaatctc 19

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters:         4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        Published Applications NA New:*
           1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
           2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
           3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
           4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
           5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
           6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
           7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
           8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
           9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
          10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c c	1	17	89.5	631	8	US-11-266-748A-360975	Sequence 360975,
	2	17	89.5	631	8	US-11-266-748A-444354	Sequence 444354,
c	3	16.4	86.3	411	8	US-11-266-748A-421952	Sequence 421952, A
	4	16.4	86.3	485	8	US-11-266-748A-11619	Sequence 11619, A
c	5	16.4	86.3	485	8	US-11-266-748A-64384	Sequence 64384, A
	6	16.4	86.3	485	8	US-11-266-748A-67216	Sequence 67216, A
	7	16.4	86.3	941	8	US-11-266-748A-188139	Sequence 188139,
c	8	16.4	86.3	941	8	US-11-266-748A-242236	Sequence 242236,
c c	9	16.4	86.3	2130	8	US-11-266-748A-74318	Sequence 74318, A
	10	16.4	86.3	2130	8	US-11-266-748A-127129	Sequence 127129,
c c	11	16.4	86.3	5175	6	US-10-547-530-4	Sequence 4, Appli
	12	16.4	86.3	5211	6	US-10-547-530-53	Sequence 53, Appl
	13	16.4	86.3	5463	6	US-10-547-530-57	Sequence 57, Appl
	14	16.4	86.3	5565	6	US-10-547-530-65	Sequence 65, Appl
c c	15	16.4	86.3	5889	6	US-10-547-530-61	Sequence 61, Appl
	16	16.4	86.3	6825	6	US-10-547-530-71	Sequence 71, Appl
c c	17	16.4	86.3	40173	8	US-11-266-748A-29048	Sequence 29048, A
	18	16	84.2	939	8	US-11-266-748A-171169	Sequence 171169,
c	19	16	84.2	1358	8	US-11-266-748A-256796	Sequence 256796,
	20	16	84.2	1358	8	US-11-266-748A-317313	Sequence 317313,
c	21	16	84.2	1370	8	US-11-266-748A-171170	Sequence 171170,
c c	22	16	84.2	1373	8	US-11-266-748A-4178	Sequence 4178, Ap
c c	23	16	84.2	2231	8	US-11-266-748A-78060	Sequence 78060, A
c c	24	16	84.2	2231	8	US-11-266-748A-130871	Sequence 130871,
c c	25	16	84.2	2958	8	US-11-266-748A-27310	Sequence 27310, A
	26	16	84.2	3400	8	US-11-266-748A-30321	Sequence 30321, A
	27	15.8	83.2	25	9	US-11-348-413-677830	Sequence 677830,
	28	15.8	83.2	25	9	US-11-348-413-677831	Sequence 677831,
	29	15.8	83.2	302	8	US-11-266-748A-2016	Sequence 2016, Ap
	30	15.8	83.2	848	8	US-11-266-748A-178638	Sequence 178638,
c	31	15.8	83.2	1968	8	US-11-218-305-18096	Sequence 18096, A
	32	15.8	83.2	39638	8	US-11-266-748A-23809	Sequence 23809, A
	33	15.8	83.2	128361	6	US-10-505-928-151	Sequence 151, App
c	34	15.8	83.2	1421559	8	US-11-266-748A-28208	Sequence 28208, A
c	35	15.4	81.1	304	8	US-11-266-748A-166770	Sequence 166770,
c	36	15.4	81.1	473	8	US-11-266-748A-300328	Sequence 300328,
c	37	15.4	81.1	990	9	US-11-348-413-634	Sequence 634, App
c	38	15.4	81.1	1245	8	US-11-266-748A-185143	Sequence 185143,
c	39	15.4	81.1	1245	8	US-11-266-748A-192633	Sequence 192633,
	40	15.4	81.1	1245	8	US-11-266-748A-240771	Sequence 240771, A
c	41	15.4	81.1	1251	9	US-11-056-355B-90108	Sequence 90108, A
c	42	15.4	81.1	1251	9	US-11-056-355B-93864	Sequence 93864, A
	43	15.4	81.1	1658	8	US-11-266-748A-185142	Sequence 185142,
c	44	15.4	81.1	1658	8	US-11-266-748A-240770	Sequence 240770, A
c	45	15.4	81.1	2043	6	US-10-953-349-25266	Sequence 25266, A

ALIGNMENTS

OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2006   Biocceleration Ltd.   GenCore version 5.1.9

Run on: August 17, 2006, 05:46:51 ; Search time 218.255 Seconds
                         (without alignments)
                         4868.007 Million cell updates/sec

Title: US-10-600-642A-5
Perfect score: 19
Sequence: 1 ccatcctctgaaaatctc 19
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
               10: gb_est9:*
               11: gb_gss1:*
               12: gb_gss2:*
               13: gb_gss3:*
               14: gb_gss4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match Length	DB	ID	Description
1	100.0	921	7	BE965735	BE965735 601659794
2	94.7	724	9	DN879125	DN879125 nae24h10.
3	17.4	115	11	AY203370	AY203370 AY203370
4	17.4	276	7	BB295113	BB295113 BB295113
5	17.4	394	5	CJ282616	CJ282616 CJ282616
6	17.4	430	12	BZ779062	BZ779062 ih86d03.g
7	17.4	445	11	AQ617138	AQ617138 HS_5158_A
8	17.4	482	7	BE353220	BE353220 EST400352
9	17.4	527	12	CB447341	CB447341 tigr-gss-
10	17.4	548	2	BI423416	BI423416 EST534082
11	17.4	589	8	CV524665	CV524665 Mdlv2_402
12	17.4	613	8	BJ188256	BJ188256 BJ188256
13	17.4	628	10	DT595457	DT595457 sheo1-9ms
14	17.4	629	1	AL703784	AL703784 DKFZp6861
15	17.4	644	11	BH015400	BH015400 TDGCA41TH
16	17.4	644	7	AW931562	AW931562 EST357405
17	17.4	684	7	AW218125	AW218125 EST303306
18	17.4	746	8	CV502261	CV502261 68642.1 M
19	17.4	748	9	CX759904	CX759904 AGENCOURT

ALIGNMENTS

20	17.4	91.6	783	14	BX968075	BX968075 Forward s
21	17.4	91.6	802	3	BQ506745	BQ506745 EST614160
22	17.4	91.6	813	10	DT582372	DT582372 sheo1-5ms
23	17.4	91.6	848	14	CT318335	CT318335 Sus scrof
24	17.4	91.6	867	14	AG837463	AG837463 Oryza sat
25	17.4	91.6	878	5	CK248403	CK248403 EST732040
26	17.4	91.6	914	14	DU948828	DU948828 399018 To
27	17.4	91.6	2244	13	CL946607	CL946607 ObiFSB005
28	17.4	91.6	355	1	AA446265	AA446265 zw60h11.s
29	17	89.5	383	10	T26578	T26578 AB325A1R In
30	17	89.5	458	11	AQ701345	AQ701345 HS_2133_A
31	17	89.5	473	1	AL135682	AL135682 DKFZp7620
32	17	89.5	502	9	DA146221	DA146221 DA146221
33	17	89.5	505	11	AZ430402	AZ430402 1M0214D20
34	17	89.5	527	9	DA175599	DA175599 DA175599
35	17	89.5	549	9	DA552897	DA552897 DA552897
36	17	89.5	551	14	CT048243	CT048243 Sus scrof
37	17	89.5	555	9	DB005316	DB005316 DB005316
38	17	89.5	560	9	DB108010	DB108010 DB108010
39	17	89.5	569	9	DA875421	DA875421 DA875421
40	17	89.5	571	9	DA157867	DA157867 DA157867
41	17	89.5	574	9	DA133385	DA133385 DA133385
42	17	89.5	575	9	DA354964	DA354964 DA354964
43	17	89.5	575	9	DA765933	DA765933 DA765933
44	17	89.5	579	9	DA091280	DA091280 DA091280
45	17	89.5	590	9	DA283653	DA283653 DA283653

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OM nucleic - nucleic search, using sw model

Run on:   August 17, 2006, 05:39:06 ; Search time 228.729 Seconds
                                      (without alignments)
                                      5591.547 Million cell updates/sec

Title:          US-10-600-642A-6
Perfect score:  19.6
Sequence:       1 tctcyctcacaagtttggc 20

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 3197371710525 residues

Total number of hits satisfying chosen parameters:     12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    GenEmbl:*
               1: gb_env:*
               2: gb_pat:*
               3: gb_ph:*
               4: gb_pl:*
               5: gb_pr:*
               6: gb_ro:*
               7: gb_sts:*
               8: gb_sy:*
               9: gb_un:*
              10: gb_vi:*
              11: gb_ov:*
              12: gb_htg:*
              13: gb_in:*
              14: gb_om:*
              15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

C	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19.6	100.0	442	2	B54412	B54412 Specific an
c	2	19.6	100.0	442	2	AR408839	AR408839 Sequence
c	3	19.6	100.0	442	15	AB022064	AB022064 Pectinatu
c	4	19.6	100.0	624	2	E54411	E54411 Specific an
c	5	19.6	100.0	624	2	AR408838	AR408838 Sequence
c	6	19.6	100.0	624	15	AB022063	AB022063 Pectinatu
	7	19.6	100.0	160383	6	AC163994	AC163994 Mus muscu
	8	19.6	100.0	171181	6	AC101796	AC101796 Mus muscu
	9	18.4	93.9	20	2	E54416	E54416 Specific an
	10	18.4	93.9	20	2	AR408843	AR408843 Sequence
	11	18	91.8	59805	12	AC101664	AC101664 Mus muscu
c	12	18	91.8	190750	6	AC116322	AC116322 Mus muscu
c	13	18	91.8	216807	12	AC174477	AC174477 Mus muscu
	14	17.6	89.8	110000	4	AP008208_006	Continuation (7 of
c	15	17.6	89.8	110000	12	AC171053_0	AC171053 Bos tauru
c	16	17.6	89.8	110000	12	AC171053_1	Continuation (2 of
c	17	17.6	89.8	150597	12	AP005005	AP005005 Oryza sat
c	18	17.6	89.8	156603	4	AP004752	AP004752 Oryza sat
c	19	17.6	89.8	220110	12	AC162023	AC162023 Bos tauru
	20	17	86.7	816	7	BV647532	BV647532 S215P6174
c	21	17	86.7	964	6	GPA536353	AJ536353 Graphiuru
c	22	17	86.7	966	6	GLO536356	AJ536356 Graphiuru
c	23	17	86.7	4197	5	HSM803592	AL833285 Homo sapi
c	24	17	86.7	7096	5	AB061835	AB061835 Homo sapi
	25	17	86.7	62001	12	AC015206	AC015206 Drosophil
	26	17	86.7	79622	12	AC036119	AC036119 Homo sapi
	27	17	86.7	90050	12	AC172645	AC172645 Bos tauru
c	28	17	86.7	110000	4	AP007159_15	Continuation (16 o
c	29	17	86.7	110000	12	AC171143_2	Continuation (3 of
c	30	17	86.7	110724	5	AC099063	AC099063 Homo sapi
	31	17	86.7	115681	12	AC158694	AC158694 Bos tauru
c	32	17	86.7	121023	14	DQ020489	DQ020489 Sus scrof
	33	17	86.7	126281	5	HS223B1	AL031943 Human DNA
	34	17	86.7	133195	11	AL935052	AL935052 Zebrafish
	35	17	86.7	134210	5	AC005052	AC005052 Homo sapi
	36	17	86.7	138641	5	AL513348	AL513348 Human DNA
	37	17	86.7	143251	11	BX510924	BX510924 Zebrafish
	38	17	86.7	151959	12	AC021689	AC021689 Homo sapi
c	39	17	86.7	153072	12	CT573036	CT573036 Mus muscu
c	40	17	86.7	154948	12	AC141985	AC141985 Rattus no
	41	17	86.7	156127	12	AC160233	AC160233 Rhinoloph
	42	17	86.7	159561	12	AC159955	AC159955 Rhinoloph
c	43	17	86.7	159981	5	AC016817	AC016817 Homo sapi
	44	17	86.7	166176	12	AC104143	AC104143 Drosophil
	45	17	86.7	167336	12	AC021350	AC021350 Homo sapi

ALIGNMENTS

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OM nucleic - nucleic search, using sw model


Run on:     August 17, 2006, 05:30:09 ; Search time 28.9067 Seconds
                                         (without alignments)
                                         4823.973 Million cell updates/sec


Title:          US-10-600-642A-6
Perfect score:  19.6
Sequence:       1 tctcytctcacaagtttggc 20

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:   544920 segs, 348612231 residues

Total number of hits satisfying chosen parameters:        10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :    N_Geneseq_8:*
          1:  geneseqn1980s:*
          2:  geneseqn1990s:*
          3:  geneseqn2000s:*
          4:  geneseqn2001as:*
          5:  geneseqn2001bs:*
          6:  geneseqn2002as:*
          7:  geneseqn2002bs:*
          8:  geneseqn2003as:*
          9:  geneseqn2003bs:*
         10:  geneseqn2003cs:*
         11:  geneseqn2003ds:*
         12:  geneseqn2004as:*
         13:  geneseqn2004bs:*
         14:  geneseqn2005s:*
         15:  geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19.6	100.0	442	3	AAZ91772	Aaz91772 Spacer re
c	2	19.6	100.0	442	4	AAI71856	Aai71856 Pectinatu
c	3	19.6	100.0	624	3	AAZ91771	Aaz91771 Spacer re
c	4	19.6	100.0	624	4	AAI71855	Aai71855 Pectinatu
	5	18.4	93.9	20	3	AAZ91776	Aaz91776 Spacer re
	6	18.4	93.9	20	4	AAI71860	Aai71860 Pectinatu
c	7	17	86.7	2126	10	ADC30432	Adc30432 Human nov
c	8	16.8	85.7	520	10	ADB56829	Adb56829 Toxicity-
c	9	16.8	85.7	520	13	ADV40260	Adv40260 Rat cardi
c	10	16.6	84.7	42104	11	ACN44606	Acn44606 Human gen
c	11	16.4	83.7	665	10	ADC77280	Adc77280 DNA homol
	12	16.4	83.7	665	10	ADK57163	Adk57163 Plant DNA
	13	16.4	83.7	665	10	ADK57378	Adk57378 Plant DNA
	14	16.4	83.7	665	10	ADK59919	Adk59919 Plant DNA
	15	16.4	83.7	667	10	ADC76706	Adc76706 DNA homol
	16	16.4	83.7	1672	13	ADX60600	Adx60600 Plant ful
	17	16.4	83.7	2000	6	ABZ15692	Abz15692 Arabidops
c	18	16.4	83.7	92099	14	ADZ12547	Adz12547 Murine ca
c	19	16.4	83.7	178825	11	ACN45144	Acn45144 Mouse gen
c	20	16.4	83.7	188267	14	ADZ13837	Adz13837 Human can
c	21	16.4	83.7	188794	12	ADQ59476	Adq59476 Human can
c	22	16	81.6	258	6	ABN76996	Abn76996 Human nuc
c	23	16	81.6	408	12	ADJ83967	Adj83967 Human asp
c	24	16	81.6	414	12	ADJ83963	Adj83963 Human asp
c	25	16	81.6	427	3	AAC27951	Aac27951 Human sec
c	26	16	81.6	465	12	ADJ83971	Adj83971 Human asp
c	27	16	81.6	516	12	ADJ83969	Adj83969 Human asp
	28	16	81.6	547	6	ABQ55556	Abq55556 Human ova
	29	16	81.6	777	6	ADJ83961	Adj83961 Human asp
	30	16	81.6	952	6	ABL55149	Abl55149 Human cyt
	31	16	81.6	1029	12	ADJ83962	Adj83962 Human asp
	32	16	81.6	1450	10	ADC30297	Adc30297 Human nov
	33	16	81.6	1695	10	ADJ46102	Adj46102 Human epi
	34	16	81.6	2168	10	ADA53116	Ada53116 Human cod
	35	16	81.6	2334	2	AAV18481	Aav18481 Human zin
	36	16	81.6	2561	2	AAV29269	Aav29269 Nucleotid
	37	16	81.6	2561	6	ABT11028	Abt11028 Human bre
	38	16	81.6	2561	6	ADS73151	Ads73151 Human kid
	39	16	81.6	2561	7	ADW42005	Adw42005 cDNA elev
	40	16	81.6	2561	15	AEF74641	Aef74641 Human pol
	41	16	81.6	2738	2	AAZ33549	Aaz33549 Human bre
	42	16	81.6	2790	2	AAV18480	Aav18480 BOP1 cDNA
	43	16	81.6	2828	6	ABN86525	Abn86525 Nucleotid
	44	16	81.6	2828	12	ADQ95837	Adq95837 T cell ac
	45	16	81.6	3975	6	ABN86526	Abn86526 Nucleotid

ALIGNMENTS

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:57:34 ; Search time 8.46222 Seconds
(without alignments)
4422.263 Million cell updates/sec

Title: US-10-600-642A-6
Perfect score: 19.6
Sequence: 1 tctcyctcacaagtttggc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Issued Patents NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1	c	19.6	100.0	442	3	US-09-762-633-2	Sequence 2, Appli
2	c	19.6	100.0	624	3	US-09-762-633-1	Sequence 1, Appli
3		18.4	93.9	20	3	US-09-762-633-6	Sequence 6, Appli
4	c	17	86.7	9110	3	US-09-949-016-13642	Sequence 13642, A
5		16.4	83.7	601	3	US-09-949-016-88998	Sequence 88998, A
6		16.4	83.7	601	3	US-09-949-016-88999	Sequence 88999, A
7	c	16.4	83.7	162465	3	US-09-949-016-14264	Sequence 14264, A
8		16	81.6	427	4	US-09-513-999C-32026	Sequence 32026, A
9	c	16	81.6	2168	4	US-10-094-749-684	Sequence 684, App
10		16	81.6	2539	2	US-09-949-016-5569	Sequence 5569, Ap
11		16	81.6	2790	2	US-08-718-661-1	Sequence 1, Appli
12		16	81.6	5385	3	US-09-920-804-1	Sequence 1, Appli
13		16	81.6	28585	3	US-09-949-016-17311	Sequence 17311, A
14	c	15.6	79.6	5621	3	US-09-566-921-106	Sequence 106, App
15		15.4	78.6	347	3	US-09-513-999C-31944	Sequence 31944, A
16		15.4	78.6	386	3	US-09-621-976-8578	Sequence 8578, Ap
17		15.4	78.6	541	3	US-09-621-976-15802	Sequence 15802, A
18	c	15.4	78.6	566	3	US-09-621-976-3389	Sequence 3389, Ap
19	c	15.4	78.6	601	3	US-09-949-016-44283	Sequence 44283, A
20	c	15.4	78.6	601	3	US-09-949-016-65452	Sequence 65452, A
21	c	15.4	78.6	601	3	US-09-949-016-146866	Sequence 146866,
22		15.4	78.6	601	3	US-09-949-016-146867	Sequence 146867,
23		15.4	78.6	601	3	US-09-949-016-146868	Sequence 146868,
24		15.4	78.6	705	3	US-09-248-796A-1497	Sequence 1497, Ap
25		15.4	78.6	1216	3	US-09-533-559-6009	Sequence 6009, Ap
26		15.4	78.6	2305	3	US-09-724-864-8	Sequence 8, Appli
27	c	15.4	78.6	17098	3	US-09-949-016-15864	Sequence 15864, A
28	c	15.4	78.6	31842	3	US-09-949-016-15123	Sequence 15123, A
29	c	15.4	78.6	60110	3	US-09-949-016-17338	Sequence 17338, A
30	c	15.4	78.6	60110	3	US-09-949-016-17339	Sequence 17339, A
31	c	15.4	78.6	61083	3	US-09-949-016-14144	Sequence 14144, A
32	c	15.4	78.6	61083	3	US-09-949-016-14145	Sequence 14145, A
33	c	15.4	78.6	87648	3	US-09-949-016-13655	Sequence 13655, A
34		15.4	78.6	95122	3	US-09-949-016-17235	Sequence 17235, A
35	c	15.4	78.6	168394	3	US-09-949-016-13002	Sequence 13002, A
36	c	15.2	77.6	291	3	US-09-313-294A-7401	Sequence 7401, Ap
37		15.2	77.6	7390	3	US-09-566-921-95	Sequence 95, Appl
38		15.2	77.6	8931	3	US-09-051-019-1	Sequence 1, Appli
39	c	15.2	77.6	263693	3	US-09-949-016-12386	Sequence 12386, A
40	c	15.2	77.6	263694	3	US-09-949-016-16915	Sequence 16915, A
41		15	76.5	25	3	US-09-396-196G-11579	Sequence 11579, A
42		15	76.5	25	3	US-09-396-196G-11580	Sequence 11580, A
43		15	76.5	25	3	US-09-396-196G-11581	Sequence 11581, A
44	c	15	76.5	300	4	US-09-297-648-2033	Sequence 2033, Ap
45		15	76.5	364	3	US-09-270-767-8345	Sequence 8345, Ap

ALIGNMENTS

```
                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:     August 17, 2006, 06:08:00 ; Search time 100.391 Seconds
                                         (without alignments)
                                         2447.953 Million cell updates/sec

Title:      US-10-600-642A-6
Perfect score: 19.6
Sequence:   1 tctcytctcacaagtttggc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:   18892170 seqs, 614381638 residues

Total number of hits satisfying chosen parameters:        37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Database : Published Applications_NA_Main:*
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 1:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US07_PUBCOMB.seq:*
 2:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
 3:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09A_PUBCOMB.seq:*
 4:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09B_PUBCOMB.seq:*
 5:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09C_PUBCOMB.seq:*
 6:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10A_PUBCOMB.seq:*
 7:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*
 8:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10C_PUBCOMB.seq:*
 9:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10D_PUBCOMB.seq:*
10:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10E_PUBCOMB.seq:*
11:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10F_PUBCOMB.seq:*
12:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10G_PUBCOMB.seq:*
13:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11A_PUBCOMB.seq:*
14:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11B_PUBCOMB.seq:*
15:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11C_PUBCOMB.seq:*
16:  /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US11D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	c	Score	Query Match %	Length	DB	ID	Description
1	c	19.6	100.0	442	8	US-10-600-642-2	Sequence 2, Appli
2	c	19.6	100.0	624	8	US-10-600-642-1	Sequence 1, Appli
3		18.4	93.9	20	8	US-10-600-642-6	Sequence 6, Appli
4		18	91.8	976	8	US-10-424-599-52516	Sequence 52516, A
5		18	91.8	1027	16	US-11-096-568A-7060	Sequence 7060, Ap
6		17	86.7	371	8	US-10-767-701-19326	Sequence 19326, A
7	c	17	86.7	376	8	US-10-424-599-130958	Sequence 130958,
8		16.6	84.7	485	4	US-09-925-065A-635628	Sequence 635628,
9		16.6	84.7	485	5	US-09-925-065A-635629	Sequence 635629,
10		16.6	84.7	485	5	US-09-925-065A-635628	Sequence 635628,
11		16.6	84.7	485	5	US-09-925-065A-635629	Sequence 635629,
12		16.6	84.7	547	5	US-09-925-065A-635630	Sequence 635630,
13		16.6	84.7	547	5	US-09-925-065A-635630	Sequence 635630,
14		16.6	84.7	550	4	US-09-925-065A-634326	Sequence 634326,
15		16.6	84.7	550	6	US-09-925-065A-634326	Sequence 634326,
16	c	16.6	84.7	42104	6	US-10-087-192-1138	Sequence 1138, Ap
17	c	16.4	83.7	488	8	US-10-424-599-110087	Sequence 110087,
18	c	16.4	83.7	539	6	US-10-027-632-140171	Sequence 140171,
19	c	16.4	83.7	539	7	US-10-027-632-140171	Sequence 140171, Ap
20		16.4	83.7	608	12	US-10-301-480-44785	Sequence 44785, A
21		16.4	83.7	608	12	US-10-301-480-658194	Sequence 658194,
22	c	16.4	83.7	615	4	US-09-925-065A-638398	Sequence 638398,
23	c	16.4	83.7	618	4	US-09-925-065A-638398	Sequence 638398,
24	c	16.4	83.7	618	5	US-09-925-065A-524353	Sequence 524353,
25	c	16.4	83.7	622	6	US-09-925-065A-524353	Sequence 524353,
26	c	16.4	83.7	622	7	US-10-027-632-185639	Sequence 185639,
27	c	16.4	83.7	665	10	US-10-027-632-185639	Sequence 185639, Ap
28		16.4	83.7	665	10	US-10-487-901-4546	Sequence 4546, Ap
29		16.4	83.7	806	10	US-10-487-901-4761	Sequence 4761, Ap
30		16.4	83.7	806	12	US-10-487-901-7302	Sequence 7302, Ap
31		16.4	83.7	966	12	US-10-301-480-597879	Sequence 597879,
32		16.4	83.7	966	4	US-10-301-480-1211288	Sequence 1211288,
33		16.4	83.7	966	4	US-09-925-065A-547753	Sequence 547753,
34		16.4	83.7	966	5	US-09-925-065A-547754	Sequence 547754,
35		16.4	83.7	966	5	US-09-925-065A-547755	Sequence 547755,
36		16.4	83.7	966	5	US-09-925-065A-547753	Sequence 547753,
37		16.4	83.7	966	12	US-09-925-065A-547754	Sequence 547754,
38		16.4	83.7	966	12	US-09-925-065A-547755	Sequence 547755,
39		16.4	83.7	966	12	US-10-301-480-525703	Sequence 525703,
40		16.4	83.7	966	12	US-10-301-480-525704	Sequence 525704,
41		16.4	83.7	966	12	US-10-301-480-525705	Sequence 525705,
42		16.4	83.7	966	12	US-10-301-480-1139112	Sequence 1139112,
43		16.4	83.7	966	12	US-10-301-480-1139113	Sequence 1139113,
44		16.4	83.7	966	12	US-10-301-480-1139114	Sequence 1139114,
45		16.4	83.7	1672	8	US-10-425-114-31443	Sequence 31443, A

ALIGNMENTS

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:    August 17, 2006, 06:09:34 ; Search time 10.7733 Seconds
                                       (without alignments)
                                       2967.635 Million cell updates/sec

Title:       US-10-600-642A-6
Perfect score: 19.6
Sequence:    1 tctcytctcacaagtttggc 20

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched:    2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters:       4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA_New:*
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             3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
             4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
             5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
             6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
             7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
             8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
             9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
            10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                           SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	91.8	1027	9	US-11-056-355B-54899	Sequence 54899, A
2	16.6	84.7	4337	8	US-11-266-748A-28282	Sequence 28282, A
3	16.4	83.7	853	9	US-11-266-748A-39712	Sequence 39712, A
4	16.4	83.7	2921	9	US-11-218-305-13146	Sequence 13146, A
5	16.4	83.7	162354	8	US-11-266-748A-23437	Sequence 23437, A
c 6	16	81.6	1000	8	US-11-266-748A-404777	Sequence 404777,
c 7	16	81.6	1000	8	US-11-266-748A-475823	Sequence 475823, A
8	16	81.6	1242	8	US-11-266-748A-26781	Sequence 26781, A
9	16	81.6	1566	8	US-11-217-529-79698	Sequence 79698, A
c 10	16	81.6	1695	6	US-10-508-063A-2	Sequence 2, Appli
c 11	16	81.6	4074	8	US-11-217-529-4467	Sequence 4467, Ap
12	16	81.6	88607	8	US-10-540-898-625	Sequence 625, App
c 13	16	81.6	185035	8	US-11-266-748A-59932	Sequence 59932, A
14	15.8	80.6	1929	6	US-10-449-902-6866	Sequence 6866, Ap
15	15.8	80.6	1942	6	US-10-449-902-27655	Sequence 27655, A
c 16	15.6	79.6	418	8	US-11-266-748A-119678	Sequence 119678,
c 17	15.6	79.6	465	8	US-11-266-748A-87744	Sequence 87744, A
18	15.6	79.6	465	8	US-11-266-748A-140555	Sequence 140555,
19	15.6	79.6	515	8	US-11-266-748A-49163	Sequence 49163, A
20	15.6	79.6	1215	9	US-11-056-355B-58762	Sequence 58762, A
c 21	15.6	79.6	1520	8	US-11-266-748A-188237	Sequence 188237,
22	15.6	79.6	1520	8	US-11-266-748A-242281	Sequence 242281,
23	15.4	78.6	427	8	US-11-266-748A-50420	Sequence 50420, A
c 24	15.4	78.6	427	8	US-11-266-748A-207588	Sequence 207588,
25	15.4	78.6	427	8	US-11-266-748A-233135	Sequence 233135,
26	15.4	78.6	695	8	US-11-266-748A-266635	Sequence 266635,
c 27	15.4	78.6	695	8	US-11-266-748A-327152	Sequence 327152,
28	15.4	78.6	1057	6	US-11-216-545-1067	Sequence 1067, Ap
c 29	15.4	78.6	1961	8	US-10-449-902-26437	Sequence 26437, A
30	15.4	78.6	2052	6	US-11-217-529-634	Sequence 634, App
c 31	15.4	78.6	2723	9	US-11-218-305-1630	Sequence 1630, Ap
32	15.4	78.6	390183	6	US-10-540-898-937	Sequence 937, App
33	15.4	78.6	634888	6	US-10-533-365-1	Sequence 1, Appli
c 34	15.2	77.6	1616	6	US-10-953-349-23939	Sequence 23939, A
c 35	15.2	77.6	1616	9	US-11-056-355B-54014	Sequence 54014, A
c 36	15.2	77.6	1959	8	US-11-216-545-4999	Sequence 4999, Ap
c 37	15.2	77.6	2011	8	US-11-216-545-5000	Sequence 5000, Ap
38	15.2	77.6	3203	8	US-11-266-748A-352168	Sequence 352168,
c 39	15.2	77.6	3203	8	US-11-266-748A-435547	Sequence 435547,
c 40	15.2	77.6	7758	6	US-10-505-928-236	Sequence 236, App
c 41	15.2	77.6	7762	8	US-11-266-748A-32565	Sequence 32565, A
42	15.2	77.6	100167	8	US-11-266-748A-61848	Sequence 61848, A
c 43	15	76.5	380	8	US-11-266-748A-374961	Sequence 374961,
44	15	76.5	380	8	US-11-266-748A-458340	Sequence 458340, A
c 45	15	76.5	461	8	US-11-266-748A-91384	Sequence 91384, A

ALIGNMENTS

```
                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:      August 17, 2006, 05:46:51 ; Search time 229.742 Seconds
                                        (without alignments)
                             4868.007 Million cell updates/sec

Title:          US-10-600-642A-6
Perfect score:  19.6
Sequence:       1 tctcyrctcacaagtttggc 20

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       48236798 segs, 2795965780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                10: gb_est9:*
                11: gb_gss1:*
                12: gb_gss2:*
                13: gb_gss3:*
                14: gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19.6	100.0	833	14	CR004625	CR004625 Forward s
2	18	91.8	440	9	BQ489531	BQ489531 76-E9231-
c 3	18	91.8	772	9	CX547812	CX547812 gmrtDrNS0
c 4	18	91.8	807	9	CX702729	CX702729 gmrtDrNS0
5	18	91.8	949	3	BU855413	BU855413 AGENCOURT
6	17.6	89.8	525	11	AQ775512	AQ775512 HS_3185_A
7	17.6	89.8	693	14	CR842343	CR842343 GR0AAA76D
c 8	17	86.7	509	7	AW755115	AW755115 PC11B04 P
c 9	17	86.7	510	9	DB322477	DB322477 DB322477
c 10	17	86.7	584	13	CW147321	CW147321 104_540_1
11	17	86.7	616	13	CW147322	CW147322 104_540_1
12	17	86.7	635	8	CO998387	CO998387 aamOI-10m
c 13	17	86.7	658	10	DR683655	DR683655 EST107373
c 14	17	86.7	664	8	CX064606	CX064606 PDUtG2091
c 15	17	86.7	667	12	BZ883851	BZ883851 CH240_189
16	17	86.7	671	4	CB002007	CB002007 VVB011H07
17	17	86.7	676	4	CB004765	CB004765 VVC005D01
c 18	17	86.7	686	3	BM764933	BM764933 K-EST0046
c 19	17	86.7	700	3	BM763755	BM763755 K-EST0045

c 20	17	86.7	705	4	BX451773	BX451773 BX451773
c 21	17	86.7	736	3	BQ635125	BQ635125 NXRV077_C
22	17	86.7	736	14	CT073182	CT073182 Sus scrof
c 23	17	86.7	738	10	DR693743	DR693743 EST108383
c 24	17	86.7	756	5	CF662726	CF662726 CcLX04a14
c 25	17	86.7	768	5	BZ168835	BZ168835 CH230-414
26	17	86.7	821	5	CK686238	CK686238 ZF101-P00
c 27	17	86.7	830	11	DU319612	DU319612 10984480 2
c 28	17	86.7	846	9	DR020109	DR020109 STRS1_34
c 29	17	86.7	853	13	DU403127	DU403127 10984482 7
c 30	17	86.7	855	10	DR687891	DR687891 EST107797
c 31	17	86.7	896	5	CK208620	CK208620 FGAS02033
c 32	17	86.7	902	14	DU889130	DU889130 387123 To
c 33	17	86.7	907	10	DT489827	DT489827 WS02543.B
34	17	86.7	937	4	BX435916	BX435916 BX435916
c 35	17	86.7	960	13	DU054235	DU054235 144670 To
c 36	17	86.7	960	13	DU094768	DU094768 109848 To
37	17	86.7	1108	5	CK209285	CK209285 FGAS02104
c 38	17	86.7	1121	5	CK208604	CK208604 FGAS02031
c 39	17	86.7	1228	6	BZ691139	BZ691139 SP_Ba000
c 40	17	85.7	1428	2	CR625387	CR625387 full-leng
c 41	17	85.7	520	1	AI103854	AI103854 EST213143
42	16.8	84.7	169	2	CC378107	CC378107 PUHBG48TB
c 43	16.6	84.7	280	2	BI032935	BI032935 MR4-NN020
c 44	16.6	84.7	425	12	BZ941497	BZ941497 CH240_92G
c 45	16.6	84.7	668	14	DU486105	DU486105 10984210 9

ALIGNMENTS

```
                 GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        August 17, 2006, 05:39:06 ; Search time 228.729 Seconds
                                          (without alignments)
                              5591.547 Million cell updates/sec

Title:         US-10-600-642A-10
Perfect score: 20
Sequence:      1 cgtatccagagatggatatt 20

Scoring table: IDENTITY NUC
               Gapop 10.0, Gapext 1.0
Searched:      6366136 seqs, 3197371 0525 residues

Total number of hits satisfying chosen parameters:    12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     GenEmbl:*
                1: gb_env:*
                2: gb_pat:*
                3: gb_ph:*
                4: gb_pl:*
                5: gb_pr:*
                6: gb_ro:*
                7: gb_sts:*
                8: gb_sy:*
                9: gb_un:*
               10: gb_vi:*
               11: gb_ov:*
               12: gb_htg:*
               13: gb_in:*
               14: gb_om:*
               15: gb_ba:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	20	2	AR034877	AR034877 Sequence
2	20	100.0	20	2	AR034887	AR034887 Sequence
3	20	100.0	20	2	E54420	E54420 Specific an
4	20	100.0	20	2	E54421	E54421 Specific an
5	20	100.0	20	2	AR408847	AR408847 Sequence
6	20	100.0	1033	1	AF530356	AF530356 Unculture
7	20	100.0	1328	1	AY916235	AY916235 Unculture
8	20	100.0	1328	1	AY975925	AY975925 Unculture
9	20	100.0	1328	1	AY976361	AY976361 Unculture
10	20	100.0	1328	1	AY980600	AY980600 Unculture
11	20	100.0	1328	1	AY981083	AY981083 Unculture
12	20	100.0	1328	1	AY982219	AY982219 Unculture
13	20	100.0	1328	1	AY982353	AY982353 Unculture
14	20	100.0	1367	15	AY428574	AY428574 Pectinatu
15	20	100.0	1449	1	AF132277	AF132277 Unculture
16	20	100.0	1498	15	AF373027	AF373027 Pectinatu
17	20	100.0	1515	1	DQ237944	DQ237944 Unculture
18	19	95.0	1412	15	AB052711	AB052711 Acetobact
19	19	95.0	1414	15	AB052710	AB052710 Acetobact
20	19	95.0	1492	1	AF349415	AF349415 Unculture
21	19	95.0	1493	1	AF349422	AF349422 Unculture
22	c 19	95.0	157430	6	AC135378	AC135378 Mus muscu
23	19	95.0	184556	6	AC117230	AC117230 Mus muscu
24	18.4	92.0	426	1	AY846114	AY846114 Unculture
25	18.4	92.0	693	1	DQ263519	DQ263519 Unculture
26	18.4	92.0	173853	6	AC154726	AC154726 Mus muscu
27	c 18.4	92.0	176213	6	CT030645	CT030645 Mouse DNA
28	18	90.0	1409	15	AP127400	AP127400 Gluconace
29	18	90.0	69947	5	AL512285	AL512285 Human DNA Continuation (7 of
30	c 18	90.0	71561	12	AL928982_6	AL928982_6
31	18	90.0	107135	5	AL008706	AL008706 Human DNA
32	c 18	90.0	124283	5	HS145B12	AC108368 Pan trogl
33	c 18	90.0	152320	5	AC084377	AC084377 Homo sapi
34	c 18	90.0	182035	12	AC068040	AC068040 Homo sapi
35	18	90.0	203185	6	AC120132	AC120132 Mus muscu
36	18	90.0	225692	12	AC165112	AC165112 Bos tauru
37	18	90.0	301967	12	AC172248	AC172248 Bos tauru
38	17.4	87.0	241	15	AY072698	AY072698 Gluconace
39	17.4	87.0	270	15	AF440747	AF440747 Asaia sp.
40	c 17.4	87.0	322	15	AY669514	AY669514 Acetobact
41	17.4	87.0	403	1	AY683282	AY683282 Unculture
42	17.4	87.0	403	1	AY683287	AY683287 Unculture
43	17.4	87.0	819	15	ASP012542	AJ012542 Acetobact
44	17.4	87.0	1004	15	AY360035	AY360035 Asaia sia
45	17.4	87.0	1137	1	AY678229	AY678229 Unculture

ALIGNMENTS

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                GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        August 17, 2006, 05:30:09 ; Search time 28.9067 Seconds
                                           (without alignments)
                                           4823.973 Million cell updates/sec

Title:         US-10-600-642A-10
Perfect score: 20
Sequence:      1 cgtatccagagatggatatt 20

Scoring table: IDENTITY_NUC
               Gapop 10.0, Gapext 1.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:   10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
```

Database :   N_Geneseq_8:*
                1: geneseqn19808:*
                2: geneseqn19908:*
                3: geneseqn20008:*
                4: geneseqn20001as:*
                5: geneseqn20001bs:*
                6: geneseqn20002as:*
                7: geneseqn20002bs:*
                8: geneseqn20003as:*
                9: geneseqn20003bs:*
               10: geneseqn20003cs:*
               11: geneseqn20003ds:*
               12: geneseqn20004as:*
               13: geneseqn20004bs:*
               14: geneseqn20005s:*
               15: geneseqn20006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES

Result   Query
No.   Score % Match Length DB ID   Description
---- ----- ------- ------ -- ---------- -----------
c 1   20   100.0   20   2 AAT69583   Aat69583 Pectinatu
   2   20   100.0   20   2 AAZ91781   Aaz91781 PCR prime
   3   20   100.0   20   3 AAZ91780   Aaz91780 PCR prime
   4   20   100.0   20   4 AAI71864   Aai71864 Pectinatu
   5   20   100.0   20   4 AAI71865   Aai71865 Pectinatu
   6   20   100.0   20   14 ADW11498   Adw11498 PCR prime
c 7   17   85.0 110000   11 ACN44932_0 Acn44932 Mouse gen
c 8   17   85.0 110000   11 ACN44932_1 Continuation (2 of
c 9 16.8   84.0   20   2 AAT69579   Aat69579 Pectinatu
  10 16.8   84.0   20   14 ADW11505   Adw11505 PCR prime
  11 16.8   82.0 128963   12 ADQ97110   Adq97110 Human can
c 12   16   80.0   251   8 ABX38205   Abx38205 Bovine ES
  13   16   80.0   652   11 ACL32681   Acl32681 Rice abio
c 14   16   80.0   948   12 ADO30434   Ado30434 Mouse GPC
  15 15.8   79.0   552   12 ADL03813   Adl03813 DNA encod
  16 15.8   79.0   588   12 ACH72375   Ach72375 Human gen
c 17 15.8   79.0   682   4 AAS43271   Aas43271 DNA encod
c 18 15.8   79.0   682   4 AAS43346   Aas43346 DNA encod
c 19 15.8   79.0   682   4 AAI85744   Aai85744 Human pol
c 20 15.8   79.0   716   3 AAF12014   Aaf12014 Aspergill
c 21 15.8   79.0   716   13 ADU56055   Adu56055 Aspergill
c 22 15.8   79.0   716   14 ADZ94058   Adz94058 Aspergill
c 23 15.8   79.0   805   8 ABZ52207   Abz52207 Aspergill
  24 15.8   79.0   1128   8 ACA24573   Aca24573 Prokaryot
c 25 15.8   79.0   1167   13 ADT47769   Adt47769 Bacterial
  26 15.8   79.0   1359   8 ACA29316   Aca29316 Prokaryot
  27 15.8   79.0   1435   13 ADX65584   Adx65584 Plant ful
  28 15.8   79.0   1470   10 ADF01029   Adf01029 Bacterial
  29 15.8   79.0   1506   11 ACH99697   Ach99697 Klebsiell
  30 15.8   79.0   9630   14 AEA61219   Aea61219 Human GPX
  31 15.8   79.0   9866   4 AAK73616   Aak73616 Human imm
c 32 15.8   79.0 12384   8 AAD48288   Aad48288 Human glu
c 33 15.8   79.0 56743   4 AAK68202   Aak68202 Human imm
c 34 15.8   79.0 56743   4 AAK81760   Aak81760 Human imm
  35 15.8   79.0 62909   8 AAF28545   Aaf28545 Genomic f
  36 15.8   79.0 110000   14 AEA61169_1 Continuation (2 of
c 37 15.8   79.0 127917   13 ADR52731   Adr52731 Drug ther
  38 15.8   79.0 133462   13 ABD32622   Abd32622 Mouse can
  39 15.4   77.0   35   9 AAL57313   Aal57313 rRNA-spec
  40 15.4   77.0   100   8 ACD70504   Acd70504 E. coli K
  41 15.4   77.0   222   2 ADA29686   Ada29686 DNA encod
  42 15.4   77.0   384   2 AAT05157   Aat05157 Dermatoph
  43 15.4   77.0   447   11 ACH96211   Ach96211 Klebsiell
  44 15.4   77.0   449   5 AAS90102   Aas90102 DNA encod
  45 15.4   77.0   1186   13 ADX59778   Adx59778 Plant ful

                         ALIGNMENTS
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OM nucleic - nucleic search, using sw model

Run on:    August 17, 2006, 05:57:34 ; Search time 8.46222 Seconds
                                        (without alignments)
                                        4422.263 Million cell updates/sec

Title:           US-10-600-642A-10
Perfect score:   20
Sequence:        1 cgtatccagagatggatatt 20

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters:    2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued Patents NA:*
            1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
            2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
            3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
            4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
            5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
            6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
            7: /EMC_Celerra_SIDS3/ptodata/2/ina/pCTUS_COMB.seq:*
            8: /EMC_Celerra_SIDS3/ptodata/2/ina/pP_COMB.seq:*
            9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
           10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	20	2	US-08-875-445-8	Sequence 8, Appli
2	20	100.0	20	2	US-08-875-445-18	Sequence 18, Appl
3	20	100.0	20	2	US-09-762-633-10	Sequence 10, Appl
c 4	16.8	84.0	20	2	US-08-875-445-4	Sequence 4, Appli
5	16.8	84.0	20	2	US-08-875-445-14	Sequence 14, Appl
6	16.8	84.0	20	2	US-09-762-633-11	Sequence 11, Appl
c 7	16	80.0	601	3	US-09-949-016-130489	Sequence 130489,
8	16	80.0	197875	3	US-09-949-016-15425	Sequence 15425, A
9	15.8	79.0	552	3	US-09-540-236-1499	Sequence 1499, Ap
10	15.8	79.0	601	3	US-09-949-016-17718	Sequence 17718, A
11	15.8	79.0	601	3	US-09-949-016-151695	Sequence 151695,
c 12	15.8	79.0	601	3	US-09-949-016-151696	Sequence 151696,
c 13	15.8	79.0	601	3	US-09-949-016-170323	Sequence 170323,
14	15.8	79.0	601	3	US-09-949-016-180600	Sequence 180600,
c 15	15.8	79.0	716	3	US-09-533-559-4537	Sequence 4537, Ap
16	15.8	79.0	1470	3	US-09-543-681A-1314	Sequence 1314, Ap
17	15.8	79.0	1506	3	US-09-489-039A-5492	Sequence 5492, Ap
18	15.8	79.0	12385	3	US-09-822-862-3	Sequence 3, Appli
c 19	15.8	79.0	46288	3	US-09-949-016-14999	Sequence 14999, A
c 20	15.8	79.0	46311	3	US-09-949-016-15000	Sequence 15000, A
21	15.8	79.0	62909	3	US-09-596-002-32	Sequence 32, Appl
c 22	15.8	79.0	87617	3	US-09-949-016-16551	Sequence 16551, A
c 23	15.8	79.0	88002	3	US-09-949-002-639	Sequence 639, App
c 24	15.8	79.0	88002	3	US-09-949-002-717	Sequence 717, App
c 25	15.8	79.0	92334	3	US-09-949-016-13920	Sequence 13920, A
c 26	15.8	79.0	92363	3	US-09-949-016-12146	Sequence 12146, A
27	15.8	79.0	98567	3	US-09-949-016-11750	Sequence 11750, A
28	15.8	79.0	100567	3	US-09-949-016-16934	Sequence 16934, A
29	15.8	79.0	283538	3	US-09-949-016-13506	Sequence 13506, A
30	15.8	79.0	317366	3	US-09-949-016-16001	Sequence 16001, A
31	15.4	77.0	222	3	US-09-328-352-973	Sequence 973, App
32	15.4	77.0	447	3	US-09-489-039A-2006	Sequence 2006, Ap
c 33	15.4	77.0	601	3	US-09-949-016-139703	Sequence 139703,
c 34	15.4	77.0	601	3	US-09-949-016-139704	Sequence 139704,
35	15.4	77.0	3012	2	US-07-991-867B-21	Sequence 21, Appl
36	15.4	77.0	3012	2	US-08-107-755A-21	Sequence 21, Appl
37	15.4	77.0	3012	2	US-08-544-332-21	Sequence 21, Appl
38	15.4	77.0	3012	2	US-09-370-861A-21	Sequence 21, Appl
39	15.4	77.0	3907	2	US-07-991-867B-33	Sequence 33, Appl
40	15.4	77.0	3907	2	US-08-107-755A-33	Sequence 33, Appl
41	15.4	77.0	3907	2	US-08-544-332-33	Sequence 33, Appl
42	15.4	77.0	3907	3	US-09-370-861A-33	Sequence 33, Appl
43	15.4	77.0	6768	2	US-08-107-755A-1	Sequence 1, Appli
44	15.4	77.0	7445	3	US-09-178-973B-8	Sequence 8, Appli
45	15.4	77.0	7445	3	US-09-419-568F-8	Sequence 8, Appli

ALIGNMENTS

```
                 GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:    August 17, 2006, 06:08:00 ; Search time 100.391 Seconds
                                        (without alignments)
                                        2447.953 Million cell updates/sec

Title:          US-10-600-642A-10
Perfect score:  20
Sequence:       1 cgtatccagagatgatt 20

Scoring table:  IDENTITY_NUC ,
                Gapop 10.0 , Gapext 1.0

Searched:       18892170 seqs, 614381763B residues

Total number of hits satisfying chosen parameters:    37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published Applications_NA_Main:*
    1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
    2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
    3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
    4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
    5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
    6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
    7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
    8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
    9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
   10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
   11:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
   12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
   13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
   14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
   15:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
   16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	%Query Match	Length	DB	ID	Description
	1	20	100.0	20	8	US-10-600-642-10	Sequence 10, Appl
c	2	17	85.0	1157	8	US-10-437-963-24506	Sequence 24506, A
c	3	17	85.0	374849	8	US-10-087-192-1627	Sequence 1627, Ap
	4	16.8	84.0	20	8	US-10-600-642-11	Sequence 11, Appl
	5	16.4	82.0	1385	10	US-10-750-185-25980	Sequence 25980, A
	6	16.4	82.0	1385	10	US-10-750-623-25980	Sequence 25980, A
	7	16.4	82.0	4584	8	US-10-437-963-88605	Sequence 88605, A
	8	16.4	82.0	21322	9	US-10-741-600-17860	Sequence 17860, A
c	9	16.4	82.0	21322	10	US-10-995-561-13418	Sequence 13418, A
	10	16.4	82.0	128963	11	US-10-330-773-86	Sequence 86, Appl
c	11	16.4	82.0	199130	9	US-10-741-600-17617	Sequence 17617, A
c	12	16.4	82.0	199130	10	US-10-995-561-13233	Sequence 13233, A
	13	16	80.0	251	3	US-09-960-352-3370	Sequence 3370, Ap
	14	16	80.0	959	9	US-10-774-355A-815	Sequence 815, App
c	15	16	80.0	966	9	US-10-774-355A-6	Sequence 6, Appli
c	16	16	80.0	966	9	US-10-774-355A-8	Sequence 8, Appli
c	17	15.8	79.0	249	9	US-10-425-115-114646	Sequence 114646,
c	18	15.8	79.0	558	12	US-10-301-480-451748	Sequence 451748,
c	19	15.8	79.0	558	12	US-10-301-480-1065157	Sequence 1065157,
	20	15.8	79.0	564	4	US-09-925-065A-741868	Sequence 741868,
	21	15.8	79.0	564	5	US-09-925-065A-741868	Sequence 741868,
	22	15.8	79.0	579	4	US-09-925-065A-382799	Sequence 382799,
c	23	15.8	79.0	579	5	US-09-925-065A-382799	Sequence 382799,
	24	15.8	79.0	588	7	US-10-029-386-5570	Sequence 5570, Ap
c	25	15.8	79.0	603	5	US-10-301-480-73397	Sequence 73397, A
c	26	15.8	79.0	603	12	US-10-301-480-686806	Sequence 686806,
c	27	15.8	79.0	614	4	US-09-925-065A-805390	Sequence 805390,
c	28	15.8	79.0	614	4	US-09-925-065A-857799	Sequence 857799,
	29	15.8	79.0	614	5	US-09-925-065A-805390	Sequence 805390,
	30	15.8	79.0	614	5	US-09-925-065A-857799	Sequence 857799,
	31	15.8	79.0	614	6	US-10-027-632-261726	Sequence 261726,
	32	15.8	79.0	614	6	US-10-027-632-261726	Sequence 261726,
	33	15.8	79.0	614	7	US-10-027-632-261727	Sequence 261727,
	34	15.8	79.0	614	7	US-10-027-632-261727	Sequence 261727,
	35	15.8	79.0	614	12	US-10-301-480-96541	Sequence 96541, A
	36	15.8	79.0	614	12	US-10-301-480-96542	Sequence 96542, A
	37	15.8	79.0	614	12	US-10-301-480-709950	Sequence 709950,
c	38	15.8	79.0	614	12	US-10-301-480-709951	Sequence 709951,
c	39	15.8	79.0	617	12	US-10-301-480-52335	Sequence 52335, A
	40	15.8	79.0	617	12	US-10-301-480-665744	Sequence 665744,
c	41	15.8	79.0	629	6	US-10-027-632-231799	Sequence 231799,
c	42	15.8	79.0	629	7	US-10-027-632-231799	Sequence 231799,
	43	15.8	79.0	637	6	US-10-027-632-197818	Sequence 197818,
c	44	15.8	79.0	637	7	US-10-027-632-197818	Sequence 197818,
c	45	15.8	79.0	649	9	US-10-425-115-182124	Sequence 182124,

ALIGNMENTS

```
OM nucleic - nucleic search, using sw model

              GenCore version 5.1.9
              Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:       August 17, 2006, 06:09:34 ; Search time 10.7733 Seconds
                                            (without alignments)
                                 2967.635 Million cell updates/sec

Title:          US-10-600-642A-10
Perfect score:  20
Sequence:       1 cgtatccagagatggatatt 20

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters:      4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published Applications NA_New:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	85.0	2917	6	US-10-449-902-24615	Sequence 24615, A
	2	16.8	84.0	1680	9	US-11-056-355B-89398	Sequence 89398, A
	3	16.8	84.0	1680	6	US-11-056-355B-93154	Sequence 93154, A
c	4	16.4	82.0	3541	6	US-10-449-902-22961	Sequence 22961, A
	5	16.4	82.0	4886	6	US-10-449-902-26413	Sequence 26413, A
	6	16.4	82.0	128963	8	US-10-540-898-86	Sequence 86, Appl
c	7	15.8	79.0	581	8	US-11-266-748A-102655	Sequence 102655,
c	8	15.8	79.0	581	8	US-11-266-748A-155466	Sequence 155466,
	9	15.8	79.0	977	8	US-11-266-748A-188281	Sequence 188281,
c	10	15.8	79.0	1149	8	US-11-266-748A-357159	Sequence 357159,
c	11	15.8	79.0	1149	8	US-11-266-748A-440538	Sequence 440538,
c	12	15.8	79.0	1167	8	US-11-217-529-78985	Sequence 78985, A
	13	15.8	79.0	1452	6	US-10-449-902-6378	Sequence 6378, Ap
	14	15.8	79.0	2182	9	US-11-218-305-13467	Sequence 13467, A
	15	15.8	79.0	4246	8	US-10-449-902-12882	Sequence 12882, A
	16	15.4	77.0	453	8	US-11-266-748A-429110	Sequence 429110,
	17	15.4	77.0	1229	9	US-11-218-305-7769	Sequence 7769, Ap
	18	15.4	77.0	2134	6	US-10-449-902-25935	Sequence 25935, A
c	19	15.4	77.0	191584	8	US-10-539-228-800	Sequence 800, App
c	20	15.2	76.0	455	8	US-11-266-748A-57868	Sequence 57868, A
	21	15.2	76.0	455	8	US-11-266-748A-209980	Sequence 209980,
c	22	15.2	76.0	455	8	US-11-266-748A-234298	Sequence 234298,
c	23	15.2	76.0	701	8	US-11-266-748A-54551	Sequence 54551, A
c	24	15.2	76.0	1000	8	US-11-266-748A-195187	Sequence 195187,
	25	15.2	76.0	1272	8	US-11-266-748A-191104	Sequence 191104,
	26	15.2	76.0	1272	8	US-11-266-748A-225629	Sequence 225629,
	27	15.2	76.0	1548	8	US-11-266-748A-183704	Sequence 183704,
	28	15.2	76.0	1548	8	US-11-266-748A-191098	Sequence 191098,
c	29	15.2	76.0	1812	9	US-11-348-413-2784	Sequence 2784, Ap
	30	15.2	76.0	2109	8	US-11-217-529-5763	Sequence 5763, Ap
	31	15.2	76.0	2356	8	US-11-266-748A-183710	Sequence 183710,
	32	15.2	76.0	2356	8	US-11-266-748A-191106	Sequence 191106,
	33	15.2	76.0	2592	8	US-11-217-529-79167	Sequence 79167, A
	34	15.2	76.0	2637	8	US-11-266-748A-20690	Sequence 20690, A
c	35	15.2	76.0	220803	8	US-11-266-748A-24865	Sequence 24865, A
	36	15.2	76.0	393323	6	US-10-540-898-23	Sequence 23, Appl
c	37	15	75.0	368	8	US-11-266-748A-37969	Sequence 37969, A
c	38	15	75.0	666	7	US-11-190-172-2885	Sequence 2885, Ap
	39	15	75.0	709	8	US-11-266-748A-171995	Sequence 171995,
c	40	15	75.0	960	8	US-11-266-748A-408954	Sequence 408954,
	41	15	75.0	1000	8	US-11-266-748A-198223	Sequence 198223,
c	42	15	75.0	1782	8	US-11-266-748A-188372	Sequence 188372,
c	43	15	75.0	2449	8	US-11-266-748A-22293	Sequence 22293, A
c	44	15	75.0	3293	8	US-11-266-748A-29845	Sequence 29845, A
	45	14.8	74.0	25	9	US-11-348-413-250457	Sequence 250457,

ALIGNMENTS

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:    August 17, 2006, 05:46:51 ; Search time 229.742 Seconds
                                        (without alignments)
                                4868.007 Million cell update/sec

Title:         US-10-600-642A-10
Perfect score: 20
Sequence:      1 cgtatcccagagatggatatt 20

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters:    96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  EST:*
       1: gb_est1:*
       2: gb_est3:*
       3: gb_est4:*
       4: gb_est5:*
       5: gb_est6:*
       6: gb_htc:*
       7: gb_est2:*
       8: gb_est7:*
       9: gb_est8:*
      10: gb_est9:*
      11: gb_gss1:*
      12: gb_gss2:*
      13: gb_gss3:*
      14: gb_gss4:*
```

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.4	87.0	327	3	BW239100	BW239100 BW239100
	2	17.4	87.0	330	3	BW241512	BW241512 BW241512
	3	17.4	87.0	339	3	BW218663	BW218663 BW218663
	4	17.4	87.0	427	10	DT586066	DT586066 aam01-40m
c	5	17.4	87.0	431	12	CC063142	CC063142 fgma002d0
c	6	17.4	87.0	442	11	AQ451583	AQ451583 HS_5157_A
c	7	17.4	87.0	555	1	AA439099	AA439099 LD13561.5
c	8	17.4	87.0	611	8	CR540685	CR540685 DKFZp459D
c	9	17.4	87.0	655	14	AG184717	AG184717 Pan trogl
	10	17.4	87.0	680	4	BX956933	BX956933 DKFZp781D
	11	17.4	87.0	734	14	AG604827	AG604827 Mus muscu
	12	17.4	87.0	759	14	CR193190	CR193190 Forward s
c	13	17.4	87.0	765	11	AQ740400	AQ740400 HS_5502_A
	14	17.4	87.0	776	9	DA572952	DA572952 DA572952
	15	17.4	87.0	796	5	CR056044	CR056044 Forward s
	16	17.4	87.0	807	9	DA572443	DA572443 DA572443
c	17	17.4	87.0	854	8	BU858483	BU858483 AGENCOURT
	18	17.4	87.0	920	14	CR025975	CR025975 Forward s
	19	17.4	87.0	955	14	CNS003HX	AL064529 Drosophil
	20	17.4	87.0	1004	14	CNS002EM	AL062407 Drosophil
	21	17.4	87.0	1148	12	CC184031	CC184031 CH261-40A
	22	17	85.0	298	4	AV038118	AV038138 AV038138
	23	17	85.0	573	4	CB212402	CB212402 OML02682
	24	17	85.0	608	8	CX112521	CX112521 EI076H17
	25	17	85.0	624	5	CK035277	CK035277 3694 8reic
	26	17	85.0	694	4	CA285680	CA285680 SCEZSD108
	27	17	85.0	714	4	CA147700	CA147700 SCEZR2101
	28	17	85.0	1016	12	CC269065	CC269065 CH261-119
c	29	16.8	84.0	393	11	B96101	B96101 F2303TRB IG
	30	16.8	84.0	481	11	AZ635587	AZ635587 1M0493B05
c	31	16.8	84.0	509	14	CR173920	CR173920 Reverse s
c	32	16.8	84.0	517	14	BX002160	BX002160 Arabidops
	33	16.8	84.0	519	11	AQ609367	AQ609367 HS_5068_B
c	34	16.8	84.0	524	11	BH205238	BH205238 Sm1-43C3.
	35	16.8	84.0	536	5	CD801621	CD801621 EST 9530
	36	16.8	84.0	539	1	AL914676	AL914676 AL914676
	37	16.8	84.0	539	1	AL914677	AL914677 AL914677
	38	16.8	84.0	549	5	CD800887	CD800887 EST 14132
	39	16.8	84.0	550	5	CD799281	CD799281 EST 12942
c	40	16.8	84.0	558	5	BQ007296	BQ007296 UI-1-BC0-
	41	16.8	84.0	578	11	BH743250	BH743250 gz71c10.g
	42	16.8	84.0	586	10	DW153237	DW153237 C1VX505.b
c	43	16.8	84.0	626	3	BU259801	BU259801 60502542
c	44	16.8	84.0	634	3	BW338401	BW338401 BW338401
	45	16.8	84.0	644	3	BU133232	BU133232 60120762

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OM nucleic - nucleic search, using sw model

Run on:     August 17, 2006, 05:39:06 ; Search time 7136.34 Seconds
                                         (without alignments)
                             5591.547 Million cell updates/sec

Title:          US-10-600-642A-1
Perfect score:  624
Sequence:       1 gaagtcgtaacaaggtagcc........agcggtatggaaagttaa 624

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       636136 seqs, 3197710525 residues

Total number of hits satisfying chosen parameters:     12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :   GenEmbl:*
         1: gb_env:*
         2: gb_pat:*
         3: gb_ph:*
         4: gb_pl:*
         5: gb_pr:*
         6: gb_ro:*
         7: gb_sts:*
         8: gb_sy:*
         9: gb_un:*
        10: gb_vi:*
        11: gb_ov:*
        12: gb_htg:*
        13: gb_in:*
        14: gb_om:*
        15: gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	624	100.0	624	2	E54411	E54411 Specific an
2	624	100.0	624	2	AR408838	AR408838 Sequence
3	624	100.0	624	15	AB022063	AB022063 Pectinatu
4	318.8	51.1	724	2	E54413	E54413 Specific an
5	318.8	51.1	724	2	AR408840	AR408840 Sequence
6	318.8	51.1	724	15	AB022061	AB022061 Pectinatu
7	318.2	51.0	442	2	E54412	E54412 Specific an
8	318.2	51.0	442	2	AR408839	AR408839 Sequence
9	318.2	51.0	442	15	AB022064	AB022064 Pectinatu
10	142.6	22.9	579	2	E34162	E34162 Gene for de
11	142.6	22.9	579	15	AB022094	AB022094 Selenomon
12	133.6	21.4	110000	15	AE015927_05	Continuation (6 of
13	132.6	21.2	5996	15	CJ16SRNA	Z29926 C.jejuni TG
14	132.6	21.2	110000	15	CP000025_00	CP000025 Campyloba
15	132.6	21.2	110000	15	CP000025_04	Continuation (5 of
16	132.6	21.2	110000	15	CP000025_07	Continuation (8 of
17	132.6	21.2	308601	15	CJ11168X2	AL139075 Campyloba
18	132.6	21.2	314150	15	CJ11168X1	AL139074 Campyloba
19	132.6	21.2	317511	15	CJ11168X3	AL139076 Campyloba
20	132.4	21.2	535	1	AY899800	AY899800 Unculture
21	129.6	20.8	417	15	AB040726	AB040726 Clostridi
c 22	128.8	20.6	6431	15	AE013169	AE013169 Thermoana
23	126.2	20.2	413	15	AB040729	AB040729 Clostridi
24	122.6	19.6	467	15	AB040727	AB040727 Clostridi
25	122.2	19.6	514	15	AB040737	AB040737 Clostridi
26	122.2	19.6	6696	15	AB045289	AB045289 Clostridi
27	122.2	19.6	7487	15	AB211985	AB211985 Campyloba
28	122.2	19.6	7878	15	AB045291	AB045291 Clostridi
c 29	122.2	19.6	110000	15	BA000016_25	Continuation (26 o
30	121	19.4	467	15	AB040730	AB040730 Clostridi
31	121	19.4	968	15	AF146727	AF146727 Campyloba
32	121	19.4	2109	1	DQ011252	DQ011252 Unculture
33	121	19.4	2110	1	DQ011251	DQ011251 Unculture
34	119	19.1	460	15	AB040723	AB040723 Clostridi
35	117.8	18.9	556	15	AB040720	AB040720 Clostridi
36	117.2	18.8	2423	15	AB066098	AB066098 Campyloba
37	117	18.8	1005	15	AJ936965	AJ936965 Xanthomon
38	117	18.8	2020	15	AY288082	AY288082 Xanthomon
39	117	18.8	2020	15	AY288083	AY288083 Xanthomon
40	117	18.8	2021	15	AY288080	AY288080 Xanthomon
41	117	18.8	2163	15	AF123093	AF123093 Xanthomon
42	117	18.8	2164	15	AF123088	AF123088 Xanthomon
43	117	18.8	2165	15	AF442743	AF442743 Xanthomon
c 44	116.8	18.7	734	1	AB198400	AB198400 Unculture
45	116.8	18.7	2020	15	AY288081	AY288081 Xanthomon

ALIGNMENTS

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                GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model
Run on:    August 17, 2006, 05:30:09 ; Search time 901.888 Seconds
                                      (without alignments)
                                      4823.973 Million cell updates/sec

Title:          US-10-600-642A-1
Perfect score:  624
Sequence:       1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 624

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:    10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_8:*
             1: geneseqn1980s:*
             2: geneseqn1990s:*
             3: geneseqn2000s:*
             4: geneseqn2001as:*
             5: geneseqn2001bs:*
             6: geneseqn2002as:*
             7: geneseqn2002bs:*
             8: geneseqn2003as:*
             9: geneseqn2003bs:*
            10: geneseqn2003cs:*
            11: geneseqn2003ds:*
            12: geneseqn2004as:*
            13: geneseqn2004bs:*
            14: geneseqn2005s:*
            15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	624	100.0	624	3	AAZ91771	Aaz91771 Spacer re
	2	624	100.0	624	4	AAI71855	Aai71855 Pectinatu
	3	318.8	51.1	724	3	AAZ91773	Aaz91773 Spacer re
	4	318.8	51.1	724	4	AAI71857	Aai71857 Pectinatu
	5	318.2	51.0	442	3	AAZ91772	Aaz91772 Spacer re
	6	318.2	51.0	442	4	AAI71856	Aai71856 Pectinatu
	7	142.6	22.9	579	3	AAA39326	Aaa39326 S. lactic
	8	116.6	18.7	399	3	AAZ91774	Aaz91774 Spacer re
	9	116.6	18.7	399	4	AAI71858	Aai71858 Pectinatu
	10	114.2	18.3	425	10	ADE11108	Ade11108 Acidovora
	11	112.4	18.0	670	10	ADE11114	Ade11114 Xanthomon
c	12	99.4	15.9	65589	6	ABA90521_23	Continuation (24 o
c	13	99.4	15.9	110000	6	ABA90521_05	Continuation (6 of
c	14	99.4	15.9	110000	6	ABA90521_19	Continuation (20 o
c	15	99.4	15.9	110000	6	ABA90521_22	Continuation (23 o
c	16	97.8	15.7	1069	6	AAX13806_	Aax13806 Enterococ
c	17	97.8	15.7	1069	6	ABS99601	Abs99601 Enterococ
c	18	91.4	14.6	681	4	AAH50334	Aah50334 Bacterial
	19	86	13.8	488	10	ADC53887	Adc53887 Pediococc
	20	85.6	13.7	339	2	AAV02628	Aav02628 S. simula
	21	84.6	13.6	479	5	AAI71400	Aai71400 Pediococc
	22	84.4	13.5	370	2	AAV78592	Aav78592 Staphyloc
c	23	84.4	13.5	400	2	AAV78196	Aav78196 Staphyloc
c	24	84.4	13.5	400	2	AAV78159	Aav78159 Staphyloc
c	25	84.4	13.5	487	2	AAV77924	Aav77924 Staphyloc
c	26	84.4	13.5	1785	2	AAV77317	Aav77317 Staphyloc
	27	84.4	13.5	5973	14	ADW94079	Adw94079 Staphyloc
	28	84.2	13.5	383	2	AAT11850	Aat11850 S. aureus
	29	84.2	13.5	460	2	AAV02624	Aav02624 S. aureus
c	30	84	13.5	323	2	AAV78650	Aav78650 Staphyloc
c	31	83	13.3	2331	14	AEB42738	Aeb42738 L. pneumo
	32	83	13.3	105295	14	AEB35712	Aeb35712 L. pneumo
	33	83	13.3	110000	14	AEB39175_04	Continuation (5 of
	34	83	13.3	110000	14	AEB39175_06	Continuation (7 of
	35	83	13.3	298667	14	AEB39173	Aeb39173 L. pneumo
c	36	82.2	13.2	240	14	AAV78887	Aav78887 Staphyloc
	37	82.2	13.2	400	2	AAV78121	Aav78121 Staphyloc
	38	81.8	13.1	195	10	ADC92601	Adc92601 E. faeciu
	39	81.4	13.0	110000	14	AEB42401_04	Continuation (5 of
	40	81.4	13.0	110000	14	AEB42401_06	Continuation (7 of
	41	79.6	12.8	1311	2	AAV77852	Aav77852 Staphyloc
	42	79.4	12.7	591	3	AAA39330	Aaa39330 Z. raffin
	43	79.2	12.7	1781	14	ACL63717	Acl63717 M. xanthu
	44	79.2	12.7	3937	4	AAH54408	Aah54408 S. epider
	45	78	12.5	7291	14	ADW94182	Adw94182 Staphyloc

ALIGNMENTS

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                      GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:    August 17, 2006, 05:57:34 ; Search time 264.021 Seconds
                                       (without alignments)
                                       4422.263 Million cell updates/sec

Title:          US-10-600-642A-1
Perfect score:  624
Sequence:       1 gaagtcgtaacaaggtagcc.........agcggttatggaagtttaa 624

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:   2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued Patents NA:*
              1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
              2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
              3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
              4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
              5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
              6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
              7: /EMC_Celerra_SIDS3/ptodata/2/ina/pCTUS_COMB.seq:*
              8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
              9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
             10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	624	100.0	624	3	US-09-762-633-1	Sequence 1, Appli
	2	318.8	51.1	724	3	US-09-762-633-3	Sequence 3, Appli
	3	318.2	51.0	442	3	US-09-762-633-2	Sequence 2, Appli
	4	116.6	18.7	399	3	US-09-762-633-4	Sequence 4, Appli
	5	85.6	13.7	339	2	US-08-607-384A-9	Sequence 9, Appli
c	6	84.4	13.5	370	3	US-08-956-171B-4281	Sequence 4281, Ap
c	7	84.4	13.5	370	3	US-08-781-986A-4281	Sequence 4281, Ap
	8	84.4	13.5	400	3	US-08-956-171B-3848	Sequence 3848, Ap
c	9	84.4	13.5	400	3	US-08-781-986A-3848	Sequence 3848, Ap
c	10	84.4	13.5	400	3	US-08-956-171B-3885	Sequence 3885, Ap
c	11	84.4	13.5	400	3	US-08-781-986A-3885	Sequence 3885, Ap
c	12	84.4	13.5	487	3	US-08-956-171B-3613	Sequence 3613, Ap
c	13	84.4	13.5	487	3	US-08-781-986A-3613	Sequence 3613, Ap
	14	84.4	13.5	1785	3	US-08-956-171B-3006	Sequence 3006, Ap
	15	84.4	13.5	1785	3	US-08-781-986A-3006	Sequence 3006, App
	16	84.2	13.5	383	3	US-08-765-332-142	Sequence 142, App
	17	84.2	13.5	383	3	US-09-448-894-142	Sequence 142, App
	18	84.2	13.5	383	3	US-09-931-486-142	Sequence 142, App
	19	84.2	13.5	460	2	US-08-607-384A-5	Sequence 5, Appli
c	20	84	13.5	323	3	US-08-956-171E-4339	Sequence 4339, Ap
c	21	84	13.5	323	3	US-08-781-986A-4339	Sequence 4339, Ap
c	22	82.4	13.2	240	3	US-08-956-171E-4576	Sequence 4576, Ap
c	23	82.4	13.2	240	3	US-08-781-986A-4576	Sequence 4576, Ap
c	24	82.2	13.2	400	3	US-08-956-171E-3810	Sequence 3810, Ap
c	25	82.2	13.2	400	3	US-08-781-986A-3810	Sequence 3810, Ap
	26	81.8	13.1	195	3	US-09-107-532A-2228	Sequence 2228, Ap
	27	79.6	12.8	1311	3	US-08-956-171E-3541	Sequence 3541, Ap
	28	79.6	12.8	1311	3	US-08-781-986A-3541	Sequence 3541, Ap
	29	79.2	12.7	1781	3	US-09-902-540-180	Sequence 180, App
	30	79.2	12.7	3937	3	US-09-710-279-3772	Sequence 3772, Ap
	31	76.6	12.3	343	3	US-08-956-171E-4181	Sequence 4181, Ap
	32	76.6	12.3	343	3	US-08-781-986A-4181	Sequence 4181, Ap
c	33	76.6	12.3	400	3	US-08-956-171E-3583	Sequence 3583, Ap
	34	76.6	12.3	400	3	US-08-956-171E-3591	Sequence 3591, Ap
c	35	76.6	12.3	400	3	US-08-956-171E-3608	Sequence 3608, Ap
c	36	76.6	12.3	400	3	US-08-956-171E-3643	Sequence 3643, Ap
	37	76.6	12.3	400	3	US-08-956-171E-3711	Sequence 3711, Ap
	38	76.6	12.3	400	3	US-08-781-986A-3583	Sequence 3583, Ap
c	39	76.6	12.3	400	3	US-08-781-986A-3591	Sequence 3591, Ap
c	40	76.6	12.3	400	3	US-08-781-986A-3608	Sequence 3608, Ap
c	41	76.6	12.3	400	3	US-08-781-986A-3643	Sequence 3643, Ap
	42	76.6	12.3	400	3	US-08-781-986A-3711	Sequence 3711, Ap
c	43	76.2	12.2	381	3	US-08-781-986A-3754	Sequence 3754, Ap
c	44	76.2	12.2	381	3	US-08-956-171E-3754	Sequence 3754, Ap
c	45	75.6	12.1	400	3	US-08-956-171E-3821	Sequence 3821, Ap

ALIGNMENTS

```
                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:     August 17, 2006, 06:08:00 ; Search time 3132.2 seconds
                                          (without alignments)
                                          2447.953 Million cell updates/sec

Title:          US-10-600-642A-1
Perfect score:  624
Sequence:       1 gaagtcgtaacaaggtagcc.........agcggttatggaaagtttaa 624

Scoring table:  IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:        37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :     Published_Applications_NA_Main:*
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          3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
          5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
          6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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         13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
         14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
         15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
         16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		624	100.0	624	8	US-10-600-642-1	Sequence 1, Appli
2		318.8	51.1	724	8	US-10-600-642-3	Sequence 3, Appli
3		318.2	51.0	442	8	US-10-600-642-2	Sequence 2, Appli
4		116.6	18.7	399	8	US-10-600-642-4	Sequence 4, Appli
5		114.2	18.3	425	7	US-10-397-551-32	Sequence 32, Appl
6		114.2	18.3	425	13	US-11-112-257-32	Sequence 32, Appl
7		112.4	18.0	670	7	US-10-397-551-38	Sequence 38, Appl
8		112.4	18.0	670	13	US-11-112-257-38	Sequence 38, Appli
9		111	17.8	2731748	8	US-10-297-465A-1	Sequence 1, Appli
10	c	97.8	15.7	1069	3	US-09-070-927A-869	Sequence 869, App
11	c	84.4	13.5	370	2	US-08-781-986A-4281	Sequence 4281, Ap
12	c	84.4	13.5	370	8	US-10-329-624-4281	Sequence 4281, Ap
13	c	84.4	13.5	400	2	US-08-781-986A-3848	Sequence 3848, Ap
14	c	84.4	13.5	400	2	US-08-781-986A-3885	Sequence 3885, Ap
15	c	84.4	13.5	400	8	US-10-329-624-3848	Sequence 3848, Ap
16	c	84.4	13.5	400	8	US-10-329-624-3885	Sequence 3885, Ap
17	c	84.4	13.5	487	2	US-08-781-986A-3613	Sequence 3613, Ap
18	c	84.4	13.5	487	8	US-10-329-624-3613	Sequence 3613, Ap
19		84.4	13.5	1785	2	US-08-781-986A-3006	Sequence 3006, Ap
20		84.4	13.5	1785	8	US-10-329-624-3006	Sequence 3006, Ap
21		84.4	13.5	5973	9	US-10-857-625-13	Sequence 13, Appl
22		84.2	13.5	383	3	US-09-931-486-142	Sequence 142, App
23		84.2	13.5	383	10	US-10-895-114-142	Sequence 142, App
24	c	84	13.5	323	2	US-08-781-986A-4339	Sequence 4339, Ap
25	c	84	13.2	323	8	US-10-329-624-4339	Sequence 4339, Ap
26	c	82.4	13.2	240	2	US-08-781-986A-4576	Sequence 4576, Ap
27	c	82.4	13.2	240	8	US-10-329-624-4576	Sequence 4576, Ap
28	c	82.2	13.2	400	2	US-08-781-986A-3810	Sequence 3810, Ap
29	c	82.2	13.2	400	8	US-10-329-624-3810	Sequence 3810, Ap
30		79.6	12.8	1311	2	US-08-781-986A-3541	Sequence 3541, Ap
31		79.6	12.8	1311	8	US-10-329-624-3541	Sequence 3541, Ap
32		79.2	12.7	3937	10	US-10-793-626-3772	Sequence 3772, Ap
33	c	78	12.5	7291	9	US-10-857-625-116	Sequence 116, App
34	c	76.6	12.3	255	3	US-09-815-242-1377	Sequence 1377, Ap
35	c	76.6	12.3	255	3	US-09-815-242-1402	Sequence 1402, Ap
36	c	76.6	12.3	255	3	US-09-815-242-1415	Sequence 1415, Ap
37	c	76.6	12.3	255	3	US-09-815-242-1423	Sequence 1423, Ap
38	c	76.6	12.3	255	3	US-09-815-242-1431	Sequence 1431, Ap
39	c	76.6	12.3	255	3	US-09-815-242-1454	Sequence 1454, Ap
40	c	76.6	12.3	255	3	US-09-815-242-1459	Sequence 1459, Ap
41	c	76.6	12.3	255	3	US-09-815-242-1473	Sequence 1473, Ap
42	c	76.6	12.3	255	3	US-09-815-242-1475	Sequence 1475, Ap
43	c	76.6	12.3	255	3	US-09-815-242-1544	Sequence 1544, Ap
44	c	76.6	12.3	255	3	US-09-815-242-1638	Sequence 1638, Ap
45		76.6	12.3	343	2	US-08-781-986A-4181	Sequence 4181, Ap

ALIGNMENTS

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              GenCore version 5.1.9
       Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   August 17, 2006, 06:09:34 ; Search time 336.128 Seconds
                                (without alignments)
                                2967.635 Million cell updates/sec

Title:          US-10-600-642A-1
Perfect score:  624
Sequence:   1 gaagtcgtaacaaggtagcc.........agcggttatggaaagtttaa 624

Scoring table:  IDENTITY_NUC
                Gapop 10.0, Gapext 1.0

Searched:       2226170 seqs, 79928156 residues

Total number of hits satisfying chosen parameters:        4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA New:*
    1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
    3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
    4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
    6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
    7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
    8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
    9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
   10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	75.8	12.1	26683	9	US-11-021-837-26	Sequence 26, Appl
2	70.6	11.3	77	9	US-11-348-413-10826	Sequence 10826, A
c 3	68	10.9	39013	8	US-11-021-837-30	Sequence 30, Appl
4	66	10.6	556	8	US-11-238-162-10	Sequence 10, Appl
5	66	10.6	603	8	US-11-238-162-11	Sequence 11, Appl
6	65.8	10.5	201	8	US-11-238-748A-416742	Sequence 416742,
7	62.6	10.1	472	8	US-11-238-162-5	Sequence 5, Appl
c 8	62.6	10.0	274050	6	US-10-550-787-5	Sequence 5, Appl
9	62.4	10.0	471	8	US-11-238-162-4	Sequence 4, Appl
10	62.4	10.0	473	8	US-11-238-162-3	Sequence 3, Appl
11	61	9.8	584	8	US-11-238-162-7	Sequence 7, Appl
12	60.2	9.6	503	8	US-11-266-748A-206328	Sequence 206328,
13	60	9.6	4294	9	US-11-021-837-14	Sequence 14, Appl
14	57.4	9.2	77	8	US-11-348-413-18	Sequence 18, Appl
15	57.2	9.2	536	8	US-11-256-428-67	Sequence 67, Appl
16	56	9.0	17395	9	US-11-021-837-52	Sequence 52, Appl
17	55.2	8.8	76	9	US-11-348-413-10833	Sequence 10833, A
18	52.8	8.5	1554	8	US-11-348-413-10825	Sequence 10825, A
19	52.4	8.4	1000	8	US-11-266-748A-206971	Sequence 206971,
c 20	52.2	8.4	1000	8	US-11-266-748A-206292	Sequence 206292,
21	50.4	8.1	76	9	US-11-348-413-1	Sequence 1, Appli
c 22	49.6	7.9	228	9	US-11-348-413-13042	Sequence 13042, A
c 23	47.2	7.6	76	9	US-11-348-413-10842	Sequence 10842, A
24	47.2	7.6	21159	9	US-11-021-837-18	Sequence 18, Appl
25	46.8	7.5	1950	6	US-10-449-902-2950	Sequence 2950, Ap
26	46.6	7.5	1538	6	US-11-348-413-12	Sequence 12, Appl
27	44.6	7.1	1452	6	US-10-511-345A-1	Sequence 1, Appli
28	44.6	7.1	1531	9	US-11-256-221-1	Sequence 1, Appli
29	44.2	7.1	5048	7	US-11-338-847-2	Sequence 2, Appli
30	43.6	7.0	73	9	US-11-348-413-2	Sequence 2, Appli
31	42	6.7	1000	8	US-11-233-726-40	Sequence 40, Appl
32	41.8	6.7	704	8	US-11-266-748A-195038	Sequence 195038,
33	41.4	6.6	1526	9	US-11-350-955-4	Sequence 4, Appl
34	41.4	6.6	1526	9	US-11-350-796-4	Sequence 4, Appl
35	41.4	6.6	1528	9	US-11-350-955-2	Sequence 2, Appli
36	41.4	6.6	1528	9	US-11-350-796-2	Sequence 2, Appli
37	41.4	6.6	1529	9	US-11-350-955-3	Sequence 3, Appli
38	41.4	6.6	1529	9	US-11-350-796-3	Sequence 3, Appli
39	41.4	6.6	1532	9	US-11-350-955-1	Sequence 1, Appli
40	41.4	6.6	1532	9	US-11-350-796-1	Sequence 1, Appli
41	41	6.6	76	9	US-11-348-413-10846	Sequence 10846, A
42	41	6.6	902	8	US-11-266-748A-44347	Sequence 44347, A
43	41	6.6	1542	8	US-11-331-987-3	Sequence 3, Appli
44	40.4	6.5	74	9	US-11-348-413-5845	Sequence 5845, Ap
45	40.4	6.5	74	9	US-11-348-413-17141	Sequence 17141, A

ALIGNMENTS

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            GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:       August 17, 2006, 05:46:51 ; Search time 7167.96 Seconds
                                           (without alignments)
                              4868.007 Million cell updates/sec

Title:         US-10-600-642a-1
Perfect score: 624
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Searched:      4823798 seqs, 2795965780 residues
Total number of hits satisfying chosen parameters:       96473596
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    EST:*
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              2:  gb_est3:*
              3:  gb_est4:*
              4:  gb_est5:*
              5:  gb_est6:*
              6:  gb_htc:*
              7:  gb_est2:*
              8:  gb_est7:*
              9:  gb_est8:*
             10:  gb_est9:*
             11:  gb_gss1:*
             12:  gb_gss2:*
             13:  gb_gss3:*
             14:  gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	107.8	17.3	810	12	CC123417	CC123417 NDL.73C23
c	2	97.8	15.7	809	13	CZ191243	CZ191243 305 GFB00
	3	97.8	15.7	6499	11	BH771024	BH771024 LLMGtag74
	4	80.2	12.9	968	14	DU735358	DU735358 APKI3214.
	5	77.2	12.4	894	14	DU768642	DU768642 APKG1053.
	6	76.6	12.3	288	5	CD518612	CD518612 AGENCOURT
	7	74	11.9	909	14	DU748135	DU748135 ASNC417.g
c	8	70.4	11.3	351	14	AG267606	AG267606 Cyanidios
	9	69.8	11.2	928	14	DU794311	DU794311 APKH5418.
c	10	69.4	11.1	631	11	BH861078	BH861078 S14H6SP6
	11	69.4	11.1	635	11	BH861097	BH861097 B1E12T7 W
c	12	66	10.6	911	14	DU741053	DU741053 APKI6052.
	13	65.8	10.5	287	11	BH614410	BH614410 1C22AG2 S
c	14	65.2	10.4	886	14	AG879127	AG879127 Oryza sat
	15	64.6	10.4	818	11	BZ554413	BZ554413 pacs1-60
c	16	64.6	10.4	823	12	BZ566461	BZ566461 pacs2-164
c	17	64.6	10.4	1352	12	BZ577091	BZ577091 msh2_5245
c	18	64.2	10.3	261	5	CF843831	CF843831 psHB04xI
c	19	64.2	10.3	525	3	BP490032	BP490032 BP490032
c	20	63.8	10.2	639	11	AQ509640	AQ509640 nbxb0096P
c	21	63	10.1	960	14	DU778616	DU778616 ASXB2276.
c	22	62.2	10.0	371	13	CZ191241	CZ191241 328 GFB00
c	23	62.2	10.0	774	13	CL965162	CL965162 OsIFCC011
c	24	61.8	10.0	507	11	BH200120	BH200120 Sm1-57J2.
c	25	61.8	9.9	629	11	BH201541	BH201541 Sm1-57P13
	26	61	9.9	487	8	CV953459	CV953459 PWrpwa_01
	27	61	9.8	501	3	BP911902	BP911902 BP911902
	28	61	9.8	536	8	CV911301	CV911301 PE025C3 m
	29	61	9.8	563	8	CV904243	CV904243 PD044F4 m
	30	61	9.8	648	8	CV950720	CV950720 PVrpvb_42
	31	61	9.8	672	8	CV947986	CV947986 PVrpvb_11
c	32	60.2	9.6	853	14	DU783531	DU783531 HF500_06
c	33	60	9.6	1335	12	BZ576949	BZ576949 msh2_5177
	34	59.4	9.5	870	11	BZ556251	BZ556251 pacs1-60
c	35	59	9.5	390	5	CK339707	CK339707 C0862C08-
	36	59	9.5	619	1	AA680996	AA680996 SW3D9CA51
c	37	58.6	9.4	992	14	DU753122	DU753122 ASNF2962.
	38	58.4	9.4	601	11	BH861047	BH861047 N14A7T7 W
	39	58	9.3	191	11	AZ578476	AZ578476 23h03 Sho
c	40	57.8	9.3	866	14	DU783720	DU783720 HF500_12
c	41	57.8	9.3	993	14	DU752455	DU752455 ASNF2588.
c	42	57.6	9.2	868	11	BH814965	BH814965 pBPC5 Mai
c	43	57.6	9.2	1143	11	BH814966	BH814966 pBPC15 Ma
	44	57.4	9.2	723	9	DN616068	DN616068 SPMSA5 Sa
c	45	57.4	9.2	970	14	DU740944	DU740944 APKI6003.

ALIGNMENTS

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                  GenCore version 5.1.9
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 05:39:06 ; Search time 5054.91 Seconds
                                              (without alignments)
                 5591.547 Million cell updates/sec

Title:           US-10-600-642A-2
Perfect score:   442
Sequence:        1 gagtcgtaacaaggtagcc..........agcggttatggaaagttaa 442

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        636136 seqs, 3197710525 residues

Total number of hits satisfying chosen parameters:    12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		442	100.0	442	2	E54412	E54412 Specific an
2		442	100.0	442	2	AR408839	AR408839 Sequence
3		442	100.0	442	15	AB022064	AB022064 Pectinatu
4		318.2	72.0	624	2	E54411	E54411 Specific an
5		318.2	72.0	624	2	AR408838	AR408838 Sequence
6		318.2	72.0	624	15	AB022063	AB022063 Pectinatu
7		208.6	47.2	399	2	E54414	E54414 Specific an
8		208.6	47.2	399	2	AR408841	AR408841 Sequence
9		208.6	47.2	399	15	AB022062	AB022062 Pectinatu
10		163.8	37.1	724	2	E54413	E54413 Specific an
11		163.8	37.1	724	2	AR408840	AR408840 Sequence
12		163.8	37.1	724	15	AB022061	AB022061 Pectinatu
13		77.4	17.5	520	15	AF080100	AF080100 Lactobaci
14		74.6	16.9	1875	15	EDI301829	AJ301829 Enterococ
15		74.4	16.8	1701	15	EMA301835	AJ301835 Enterococ
16		70.6	16.0	3328	15	AF401673	AF401673 Lactobaci
17	c	70.6	16.0	84661	15	CR936503_18	Continuation (19 o
18	c	70.6	16.0	110000	15	CR936503_02	Continuation (3 of
19		70.6	16.0	110000	15	CR936503_03	Continuation (4 of
20		70.6	16.0	110000	15	CR936503_04	Continuation (5 of
21		70.6	16.0	110000	15	CR936503_15	Continuation (16 o
22	c	69	15.6	284	2	BD01456	BD01456 Oligonucl
23		69	15.6	477	1	AB198420	AB198420 Unculture
24	c	68.2	15.4	7218	2	I66494	I66494 Sequence 14
25		68	15.4	560	15	AF429604	AF429604 Lactobaci
26		67.8	15.3	474	15	AF478106	AF478106 Paenibaci
27		67.8	15.3	528	15	AF405382	AF405382 Pediococc
28		67.8	15.3	534	15	AF405366	AF405366 Pediococc
29		67.8	15.3	534	15	AF405384	AF405384 Pediococc
30		67.6	15.3	534	15	AF405367	AF405367 Pediococc
31		67.4	15.2	531	15	AF405365	AF405365 Pediococc
32		67.4	15.2	535	15	AF405359	AF405359 Pediococc
33		67.4	15.2	536	15	AF405358	AF405358 Pediococc
34		66.8	15.1	552	15	AB083115	AB083115 Lactobaci
35		66.8	15.1	110000	15	AB017194_03	Continuation (4 of
36		66.6	15.1	4566	15	AB019250	AB019250 Erysipelo
37		66.6	15.1	4865	15	AB019248	AB019248 Erysipelo
38		65.8	14.9	4867	15	AB019247	AB019247 Erysipelo
39		65.2	14.8	497	15	AY008265	AY008265 Bacillus
40		65.2	14.8	509	15	AF293851	AF293851 Bacillus
41		65.2	14.8	110000	15	AE016879_00	AE016879 Bacillus
42		65.2	14.8	110000	15	AE016879_01	Continuation (2 of
43		65.2	14.8	110000	15	AE016879_02	Continuation (3 of
44		65.2	14.8	110000	15	AE016879_05	Continuation (6 of
45		65.2	14.8	110000	15	AE016879_07	Continuation (8 of

ALIGNMENTS

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:30:09 ; Search time 638.837 Seconds
(without alignments)
4823.973 Million cell updates/sec

Title: US-10-600-642A-2
Perfect score: 442
Sequence: 1 gaagtcgtaacaaggtagcc.........agcggttatggaaagtttaa 442

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 348612431 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   N_Geneseq_8:*
      1: geneseqn1980s:*
      2: geneseqn1990s:*
      3: geneseqn2000s:*
      4: geneseqn2001as:*
      5: geneseqn2001bs:*
      6: geneseqn2002as:*
      7: geneseqn2002bs:*
      8: geneseqn2003as:*
      9: geneseqn2003bs:*
     10: geneseqn2003cs:*
     11: geneseqn2003ds:*
     12: geneseqn2004as:*
     13: geneseqn2004bs:*
     14: geneseqn2005s:*
     15: geneseqn2006s:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	442	100.0	442	3	AAZ91772	Aaz91772 Spacer re
	2	442	100.0	442	4	AAI71856	Aai71856 Pectinatu
	3	318.2	72.0	624	3	AAZ91771	Aaz91771 Spacer re
	4	318.2	72.0	624	4	AAI71855	Aai71855 Pectinatu
	5	208.6	47.2	399	3	AAZ91774	Aaz91774 Spacer re
	6	208.6	47.2	399	4	AAI71858	Aai71858 Pectinatu
	7	163.8	37.1	724	3	AAZ91773	Aaz91773 Spacer re
	8	163.8	37.1	724	4	AAI71857	Aai71857 Pectinatu
	9	69	15.6	284	5	AAI71401	Aai71401 Pediococc
	10	67.4	15.2	291	10	ADC53888	Adc53888 Pediococc
	11	64.2	14.5	538	13	ADU78344	Adu78344 Lactobaci
	12	63.2	14.3	753	4	AAC88675	Aac88675 Intergeni
	13	63.2	14.3	753	9	ABS52493	Abs52493 Acidovora
c	14	62.4	14.1	110000	9	ADB12064_00	Adb12064 Alloiococc
	15	62.4	14.1	110000	9	ADB12064_05	Continuation (6 of
	16	62.2	14.1	526	2	ADE11115	Adel1115 Erwinia t
c	17	61.8	14.0	1069	2	AAX13806	Aax13806 Enterococ
c	18	61.8	14.0	1069	6	ABS99601	Abs99601 Enterococ
	19	61.8	14.0	2996	12	ADH50160	Adh50160 Bacterial
	20	61.8	14.0	110000	9	ADB12064_04	Continuation (5 of
c	21	61.8	14.0	110000	9	ADB12064_14	Continuation (15 o
c	22	61.6	14.0	110000	9	ADB12064_15	Continuation (16 o
	23	61.6	13.9	414	2	AAQ62078	Aaq62078 Lactobaci
	24	61.6	13.9	414	2	AAQ88211	Aaq88211 Lactobaci
	25	61.6	13.9	540	2	AAQ62072	Aaq62072 L. hetero
	26	61.6	13.9	540	2	AAQ88205	Aaq88205 Lactobaci
	27	61.6	13.9	585	2	AAQ62079	Aaq62079 L. brevis
	28	61.6	13.9	585	2	AAQ88212	Aaq88212 Lactobaci
	29	61	13.8	614	13	ADU78345	Adu78345 Streptoco
c	30	60.8	13.8	65589	13	ABA90521_23	Continuation (24 o
	31	60.8	13.8	110000	6	ABA90521_05	Continuation (6 of
c	32	60.8	13.8	110000	6	ABA90521_19	Continuation (20 o
c	33	60.8	13.8	110000	6	ABA90521_22	Continuation (23 o
	34	60.6	13.7	294	10	ADC53892	Adc53892 Pediococc
	35	60.6	13.7	294	10	ADC53890	Adc53890 Pediococc
	36	60.6	13.7	4259	13	ADV87716	Adv87716 Streptoco
	37	60.6	13.7	4259	13	ADV78969	Adv78969 Streptoco
	38	60.6	13.7	7250	6	ABN72583	Abn72583 Streptoco
c	39	60.6	13.7	7267	6	ABN72580	Abn72580 Streptoco
c	40	60.6	13.7	7361	6	ABN72578	Abn72578 Streptoco
c	41	60.6	13.7	7392	6	ABN72582	Abn72582 Streptoco
c	42	60.6	13.7	8172	6	ABN72579	Abn72579 Streptoco
c	43	60.6	13.7	8766	6	ABN72581	Abn72581 Streptoco
c	44	60.6	13.7	9042	6	ABN72584	Abn72584 Streptoco
c	45	60.6	13.7	55561	6	ABN71527_21	Continuation (22 o

ALIGNMENTS

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.9

Run on: August 17, 2006, 05:57:34 ; Search time 187.015 Seconds
                                          (without alignments)
                                4422.263 Million cell updates/sec

Title: US-10-600-642A-2
Perfect score: 442
Sequence: 442 1 gaagtcgtaacaaggtagcc.........agcggttatgaaagttaa 442

Scoring table: IDENTITY_NUC
                  GapOp 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Match	Query Length	DB	ID	Description
1		442	100.0	442	3	US-09-762-633-2	Sequence 2, Appli
2		318.2	72.0	624	3	US-09-762-633-1	Sequence 1, Appli
3		208.6	47.2	399	3	US-09-762-633-4	Sequence 4, Appli
4		163.8	37.1	724	2	US-09-762-633-3	Sequence 3, Appli
5	c	68.2	15.4	7218	2	US-08-232-463-14	Sequence 14, Appli
6		63.2	14.3	753	3	US-09-393-877-9	Sequence 9, Appli
7		63.2	14.3	753	3	US-09-703-807-9	Sequence 9, Appli
8		60.4	13.7	261	3	US-09-583-110-1038	Sequence 1038, Ap
9		60.4	13.7	261	3	US-09-583-110-1763	Sequence 1763, Ap
10	c	60	13.6	251	3	US-08-956-171E-4521	Sequence 4521, Ap
11	c	60	13.6	251	3	US-08-781-986A-4521	Sequence 4521, Ap
12	c	60	13.6	322	3	US-08-956-171E-4395	Sequence 4395, Ap
13	c	60	13.6	322	3	US-08-781-986A-4395	Sequence 4395, Ap
14	c	60	13.6	333	3	US-08-956-171E-4473	Sequence 4473, Ap
15	c	60	13.6	333	3	US-08-781-986A-4473	Sequence 4473, Ap
16	c	60	13.6	362	3	US-08-956-171E-4147	Sequence 4147, Ap
17	c	60	13.6	362	3	US-08-781-986A-4147	Sequence 4147, Ap
18	c	60	13.6	389	3	US-08-956-171E-3950	Sequence 3950, Ap
19	c	60	13.6	389	3	US-08-781-986A-3950	Sequence 3950, Ap
20	c	60	13.6	400	3	US-08-956-171E-3583	Sequence 3583, Ap
21	c	60	13.6	400	3	US-08-956-171E-3608	Sequence 3608, Ap
22	c	60	13.6	400	3	US-08-956-171E-3617	Sequence 3617, Ap
23	c	60	13.6	400	3	US-08-956-171E-3637	Sequence 3637, Ap
24	c	60	13.6	400	3	US-08-956-171E-3689	Sequence 3689, Ap
25	c	60	13.6	400	3	US-08-956-171E-3697	Sequence 3697, Ap
26		60	13.6	400	3	US-08-956-171E-3711	Sequence 3711, Ap
27		60	13.6	400	3	US-08-956-171E-3716	Sequence 3716, Ap
28		60	13.6	400	3	US-08-956-171E-3758	Sequence 3758, Ap
29		60	13.6	400	3	US-08-956-171E-3810	Sequence 3810, Ap
30		60	13.6	400	3	US-08-956-171E-3820	Sequence 3820, Ap
31		60	13.6	400	3	US-08-956-171E-3821	Sequence 3821, Ap
32		60	13.6	400	3	US-08-956-171E-3832	Sequence 3832, Ap
33		60	13.6	400	3	US-08-956-171E-3885	Sequence 3885, Ap
34		60	13.6	400	3	US-08-956-171E-3922	Sequence 3922, Ap
35		60	13.6	400	3	US-08-956-171E-3938	Sequence 3938, Ap
36		60	13.6	400	3	US-08-956-171E-4126	Sequence 4126, Ap
37		60	13.6	400	3	US-08-781-986A-3583	Sequence 3583, Ap
38		60	13.6	400	3	US-08-781-986A-3608	Sequence 3608, Ap
39		60	13.6	400	3	US-08-781-986A-3617	Sequence 3617, Ap
40		60	13.6	400	3	US-08-781-986A-3637	Sequence 3637, Ap
41		60	13.6	400	3	US-08-781-986A-3689	Sequence 3689, Ap
42		60	13.6	400	3	US-08-781-986A-3697	Sequence 3697, Ap
43		60	13.6	400	3	US-08-781-986A-3711	Sequence 3711, Ap
44	c	60	13.6	400	3	US-08-781-986A-3716	Sequence 3716, Ap
45	c	60	13.6	400	3	US-08-781-986A-3758	Sequence 3758, Ap

ALIGNMENTS

```
                    GenCore version 5.1.9
        Copyright (c) 1993 - 2006  Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    August 17, 2006, 06:08:00 ; Search time 2218.64 Seconds
                                        (without alignments)
                                        2447.953 Million cell updates/sec

Title:           US-10-600-642A-2
Perfect score:   442
Sequence:        1 gaagtcgtaacaaggtagcc........agcggttatggaagttaa 442

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:       37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications NA Main:*
            1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
            2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
            3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
            4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
            5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
            6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
            7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
            8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
            9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
           10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
           11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
           12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
           13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
           14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
           15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
           16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	442	100.0	442	8	US-10-600-642-2	Sequence 2, Appli
	2	318.2	72.0	624	8	US-10-600-642-1	Sequence 1, Appli
	3	208.6	47.2	399	8	US-10-600-642-4	Sequence 4, Appli
	4	163.8	37.1	724	8	US-10-600-642-3	Sequence 3, Appli
	5	62.4	14.1	1754382	10	US-10-501-282-6651	Sequence 6651, Ap
c	6	62.4	14.1	1754382	10	US-10-501-282-6651	Sequence 6651, Ap
	7	62.2	14.1	526	7	US-10-397-551-39	Sequence 39, Appl
	8	62.2	14.1	526	13	US-11-112-257-39	Sequence 39, Appl
c	9	61.8	14.0	1069	3	US-09-070-927A-869	Sequence 869, App
c	10	60.4	13.7	2162598	9	US-10-472-928-4979	Sequence 4979, Ap
c	11	60.4	13.7	2162598	9	US-10-472-928-4979	Sequence 4979, Ap
c	12	60	13.6	251	8	US-08-781-986A-4521	Sequence 4521, Ap
c	13	60	13.6	251	8	US-10-329-624-4521	Sequence 4521, Ap
c	14	60	13.6	252	8	US-10-282-122A-5323	Sequence 5323, Ap
c	15	60	13.6	322	8	US-08-781-986A-4395	Sequence 4395, Ap
c	16	60	13.6	322	8	US-10-329-624-4395	Sequence 4395, Ap
c	17	60	13.6	333	2	US-08-781-986A-4473	Sequence 4473, Ap
c	18	60	13.6	333	8	US-10-329-624-4473	Sequence 4473, Ap
c	19	60	13.6	362	2	US-08-781-986A-4147	Sequence 4147, Ap
c	20	60	13.6	362	8	US-10-329-624-4147	Sequence 4147, Ap
c	21	60	13.6	379	3	US-09-815-242-2479	Sequence 2479, Ap
c	22	60	13.6	379	8	US-09-815-242-2501	Sequence 2501, Ap
c	23	60	13.6	379	8	US-10-282-122A-5007	Sequence 5007, Ap
c	24	60	13.6	379	8	US-10-282-122A-5030	Sequence 5030, Ap
c	25	60	13.6	389	8	US-08-781-986A-3950	Sequence 3950, Ap
c	26	60	13.6	389	8	US-10-329-624-3950	Sequence 3950, Ap
c	27	60	13.6	395	3	US-09-815-242-1811	Sequence 1811, Ap
c	28	60	13.6	395	3	US-09-815-242-1859	Sequence 1859, Ap
c	29	60	13.6	395	8	US-10-282-122A-4382	Sequence 4382, Ap
c	30	60	13.6	395	8	US-10-282-122A-4383	Sequence 4383, Ap
c	31	60	13.6	400	2	US-08-781-986A-3583	Sequence 3583, Ap
c	32	60	13.6	400	2	US-08-781-986A-3608	Sequence 3608, Ap
c	33	60	13.6	400	2	US-08-781-986A-3617	Sequence 3617, Ap
c	34	60	13.6	400	2	US-08-781-986A-3637	Sequence 3637, Ap
c	35	60	13.6	400	2	US-08-781-986A-3689	Sequence 3689, Ap
c	36	60	13.6	400	2	US-08-781-986A-3697	Sequence 3697, Ap
c	37	60	13.6	400	2	US-08-781-986A-3711	Sequence 3711, Ap
c	38	60	13.6	400	2	US-08-781-986A-3716	Sequence 3716, Ap
c	39	60	13.6	400	2	US-08-781-986A-3758	Sequence 3758, Ap
c	40	60	13.6	400	2	US-08-781-986A-3810	Sequence 3810, Ap
c	41	60	13.6	400	2	US-08-781-986A-3820	Sequence 3820, Ap
c	42	60	13.6	400	2	US-08-781-986A-3821	Sequence 3821, Ap
c	43	60	13.6	400	2	US-08-781-986A-3832	Sequence 3832, Ap
c	44	60	13.6	400	2	US-08-781-986A-3885	Sequence 3885, Ap
c	45	60	13.6	400	2	US-08-781-986A-3922	Sequence 3922, Ap

ALIGNMENTS

```
                                                                          c  24  38.4  8.7  2718  9  US-11-218-305-12773        Sequence 12773, A
                                                                          c  25  38.2  8.6  5976  6  US-10-517-441-554          Sequence 554, App
        GenCore version 5.1.9                                                26    38  8.6   771  6  US-11-266-748A-41252       Sequence 41252, A
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.                    c  27    38  8.6  5493  6  US-10-517-441-417          Sequence 417, App
                                                                          c  28  37.8  8.6  6001  8  US-10-517-441-777          Sequence 777, App
OM nucleic - nucleic search, using sw model                                  29  37.6  8.5  1142  9  US-11-216-545-1530         Sequence 1530, Ap
                                                                             30  37.6  8.4  4009  9  US-11-218-305-3660         Sequence 3660, Ap
Run on:    August 17, 2006, 06:09:34 ; Search time 238.091 Seconds           31  37.2  8.4  1826  9  US-11-216-545-774          Sequence 774, App
                            (without alignments)                             32    37  8.4  1175  9  US-11-218-305-18377        Sequence 18377, A
                            2967.635 Million cell updates/sec                33    37  8.4  1602  6  US-10-449-902-11377        Sequence 11377, A
                                                                             34  36.8  8.3  1399  8  US-11-266-748A-180787      Sequence 180787
Title:         US-10-600-642A-2                                           c  35  36.8  8.3  1399  9  US-11-266-748A-241095      Sequence 241095,
Perfect score: 442                                                        c  36  36.6  8.3  1581  8  US-11-056-355B-23650       Sequence 23650, A
Sequence:      1 gaagtcgtaacaaggtagcc..........agcggttatgaaagtttaa 442    c  37  36.6  8.3   896  9  US-11-266-748A-49860       Sequence 49860, A
                                                                             38  36.6  8.3  1000  8  US-11-266-748A-285975      Sequence 285975,
Scoring table: IDENTITY_NUC                                               c  39  36.6  8.3  1000  8  US-11-266-748A-290882      Sequence 290882,
               Gapop 10.0 , Gapext 1.0                                    c  40  36.6  8.3  1000  8  US-11-266-748A-337404      Sequence 337404,
                                                                             41  36.6  8.3  1000  8  US-11-266-748A-342311      Sequence 342311,
Searched:      2226170 seqs, 799283156 residues                           c  42  36.6  8.3  1000  8  US-11-266-748A-402246      Sequence 402246,
                                                                             43  36.6  8.3  1000  8  US-11-266-748A-473292      Sequence 473292,
Total number of hits satisfying chosen parameters:      4452340           c  44  36.6  8.3  2110  8  US-11-266-748A-30715       Sequence 30715, A
                                                                          c  45  36.6  8.3  2153  8  US-11-266-748A-187554      Sequence 187554,
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%                                                            ALIGNMENTS
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published Applications NA New:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
               10:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                     SUMMARIES

Result          %
No.     Score   Query Match   Length  DB  ID                          Description
-----   -----   -----------   ------  --  --                          -----------
    1      60   13.6            4294   9  US-11-021-837-14            Sequence 14, Appl
c   2      60   13.6           26683   9  US-11-021-837-26            Sequence 26, Appl
    3    52.8   11.9            1554   8  US-11-348-413-10825         Sequence 10825, A
    4    52.4   11.9            1000   8  US-11-266-748A-206971       Sequence 206971,
c   5    52.2   11.8            1000   8  US-11-266-748A-206292       Sequence 206292,
    6    46.8   10.6            1950   9  US-10-449-902-2950          Sequence 2950, Ap
    7    46.6   10.5            1538   9  US-11-348-413-12            Sequence 12, Appl
    8    44.6   10.1            1452   6  US-10-511-345A-1            Sequence 1, Appli
    9    44.6   10.1            1531   8  US-11-256-221-1             Sequence 1, Appli
   10    42.6    9.6             902   9  US-11-266-748A-44347        Sequence 44347, A
c  11    42.6    9.6          274050   6  US-10-550-787-5             Sequence 5, Appli
   12    41.8    9.5             704   8  US-11-266-748A-195038       Sequence 195038,
   13    41.4    9.4            1526   9  US-11-350-955-4             Sequence 4, Appli
   14    41.4    9.4            1526   9  US-11-350-796-4             Sequence 4, Appli
   15    41.4    9.4            1528   9  US-11-350-955-2             Sequence 2, Appli
   16    41.4    9.4            1528   9  US-11-350-796-2             Sequence 2, Appli
   17    41.4    9.4            1529   9  US-11-350-955-3             Sequence 3, Appli
   18    41.4    9.4            1529   9  US-11-350-796-3             Sequence 3, Appli
   19    41.4    9.4            1532   9  US-11-350-955-1             Sequence 1, Appli
   20    41.4    9.4            1532   9  US-11-350-796-1             Sequence 1, Appli
   21      41    9.3            1542   8  US-11-331-987-3             Sequence 3, Appli
   22    39.2    8.9            5849   8  US-11-270-287-1             Sequence 1, Appli
   23    38.8    8.8            5155   8  US-11-266-748A-28283        Sequence 28283, A
```

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            GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        August 17, 2006, 05:46:51 ; Search time 5077.3 Seconds
                                          (without alignments)
                                          4868.007 Million cell updates/sec

Title:         US-10-600-642A-2
Perfect score: 442
Sequence:      1 gaagtcgtaacaaggtagcc..........agcggttatgaaagtttaa 442

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:      48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters:     96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1: gb_est1:*
               2: gb_est3:*
               3: gb_est4:*
               4: gb_est5:*
               5: gb_est6:*
               6: gb_htc:*
               7: gb_est2:*
               8: gb_est7:*
               9: gb_est8:*
              10: gb_est9:*
              11: gb_gss1:*
              12: gb_gss2:*
              13: gb_gss3:*
              14: gb_gss4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	61.8	14.0	371	13	CZ191241	CZ191241 328 GFE00
c	2	61.8	14.0	809	13	CZ191243	CZ191243 305 GFE00
	3	60.8	13.8	6499	11	BH771024	BH771024 LLMGtag74
c	4	59	13.3	390	5	CK339707	CK339707 C0862C08-
c	5	57.6	13.0	868	11	BH814965	BH814965 pBPC5 Mai
c	6	57.6	13.0	1143	11	BH814966	BH814966 pBPC15 Ma
	7	57.4	13.0	723	9	DN616068	DN616068 SPM5A5 Sa
c	8	57.4	13.0	970	14	DU740944	DU740944 APKI6003.
c	9	56.4	12.8	781	13	CL680069	CL680069 PRI0127d_
	10	56.4	12.8	926	14	DU776044	DU776044 APKG936.g
c	11	56.2	12.7	967	14	DU750621	DU750621 ASNF1573.
	12	55.8	12.6	798	9	CX648081	CX648081 COLD1_26.
	13	55.2	12.5	364	9	DN255127	DN255127 Meso09926
	14	54.4	12.3	920	14	DU753933	DU753933 ASNF3450.
c	15	54.2	12.3	805	14	DX079498	DX079498 KBrB091L2
	16	53.8	12.2	715	9	DN256273	DN256273 Meso09925
	17	53.6	12.1	870	14	DU769019	DU769019 APKG1243.
	18	53.6	12.1	894	14	DU768642	DU768642 APKG1053.
	19	53.6	12.1	905	14	DU733926	DU733926 APKI2488.
c	20	53.2	12.0	549	5	CI175518	CI175518 CI175518
	21	52.8	11.9	1856	10	DV782961	DV782961 Hw liver.
	22	52.6	11.9	307	11	BH675535	BH675535 BOHTL47TF
	23	52.6	11.9	572	11	BH440331	BH440331 BOGGP28TF
c	24	52.6	11.9	631	11	BH861078	BH861078 S14H6SP6
	25	52.6	11.9	635	11	BH861097	BH861097 B1E12T7 W
	26	52.6	11.9	666	11	BH442635	BH442635 BOGGA26TP
	27	52.6	11.9	670	5	CD211293	CD211293 HS1_59_H0
	28	52.6	11.9	671	11	BH572139	BH572139 BOGXR35TR
	29	52.6	11.9	717	11	BH559104	BH559104 BOGZW82TR
	30	52.6	11.9	736	11	BH732230	BH732230 BOMMY63TF
c	31	52.6	11.9	757	11	BZ441299	BZ441299 BOMMN23TF
c	32	52.6	11.9	783	11	BH433849	BH433849 BOGUR44TR
c	33	52.6	11.9	801	11	BH556768	BH556768 BOGLJ11TR
c	34	52.6	11.9	810	12	CC123417	CC123417 NDL.73C23
c	35	52.6	11.9	812	11	BH431271	BH431271 BOGKJ34TF
c	36	52.6	11.9	814	11	BZ425868	BZ425868 BONCH5TF
c	37	52.6	11.9	837	11	BZ520384	BZ520384 BOMQO15TF
c	38	52.4	11.9	831	14	CT317837	CT317837 Sus scrof
c	39	52.2	11.8	351	8	CN028875	CN028875 UMC-pbliv
c	40	52.2	11.8	374	8	CN027713	CN027713 UMC-p4civ
c	41	52.2	11.8	380	8	CN027797	CN027797 UMC-p4civ
c	42	52.2	11.8	380	13	CW075218	CW075218 104_356_1
	43	52.2	11.8	500	9	DN257224	DN257224 Meso09924
	44	52.2	11.8	1571	12	CL066123	CL066123 CH216-107
	45	51.8	11.7	687	11	BZ429618	BZ429618 BONLU78TR

ALIGNMENTS

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome
limitations in most standard search systems which favor large sequences with high
scoring, but lesser overall identity over smaller sequences with higher overall identity.
This search is especially useful for relatively small nucleic acid or polypeptide target
sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed
functionally via a form of hybridization and/or identity language and having defined
upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using
examiner-specified identity and polynucleotide or protein length limit parameters, and
saving 65,000 hits and 0 alignments from each desired database. The resulting output is
reformatted using a Microsoft Word macro and is imported into Excel. The summary
table data are then sorted by the ratio of score of each hit sequence divided by its length
and the accession numbers for all hits below the examiner's desired score over length
parameters are deleted. The remaining accession numbers are used to pull the
corresponding sequences from the databases into subdatabases enriched for good hits and
the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is _70%_

Examiner Please Note: This cover sheet should be included when submitting results to
be scanned.

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                      GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          August 18, 2006, 15:23:52 ; Search time 0.001 Seconds
                                             (without alignments)
                                             1583.244 Million cell updates/sec

Title:           US-10-600-642A-2-COPY
Perfect score:   442
Sequence:        1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 442


Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5


Searched:        21 seqs, 1791 residues


Total number of hits satisfying chosen parameters:      42


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 21 summaries


Database :       gedb2:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                              SUMMARIES
                      %
Result              Query
     No.    Score  Match Length DB  ID                    Description
     -------------------------------------------------------------------------------
        1    442   100.0    442  1  E54412                ACCESSION:E54412
        2    442   100.0    442  1  AR408839              ACCESSION:AR408839
        3    442   100.0    442  1  AB022064              ACCESSION:AB022064
        4     50.4   11.4    52  1  BACRRDA               ACCESSION:M13610
        5     45.2   10.2    50  1  STMRR16S              ACCESSION:M26120
        6     26.8    6.1    30  1  CS001459              ACCESSION:CS001459
   c    7     23.8    5.4    27  1  AR124123              ACCESSION:AR124123
   c    8     23.8    5.4    27  1  AR282388              ACCESSION:AR282388
   c    9     22      5.0    22  1  CQ880246              ACCESSION:CQ880246
   c   10     22      5.0    22  1  CQ945361              ACCESSION:CQ945361
   c   11     22      5.0    22  1  E10212                ACCESSION:E10212
   c   12     21.6    4.9    22  1  AR147479              ACCESSION:AR147479
   c   13     21.6    4.9    22  1  BD078568              ACCESSION:BD078568
   c   14     21.6    4.9    22  1  AX076870              ACCESSION:AX076870
   c   15     21      4.8    21  1  BD140325              ACCESSION:BD140325
   c   16     21      4.8    21  1  CQ889258              ACCESSION:CQ889258
   c   17     20.6    4.7    21  1  BD078551              ACCESSION:BD078551
```

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C  18    20.6    4.7    21  1  BD167392          ACCESSION:BD167392
C  19    20.6    4.7    21  1  BD170790          ACCESSION:BD170790
C  20    20.6    4.7    21  1  AR234471          ACCESSION:AR234471
C  21    20.6    4.7    21  1  I57963            ACCESSION:I57963
```

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:            August 18, 2006, 15:06:04 ; Search time 1 Seconds
                                              (without alignments)
                                              7.619 Million cell updates/sec

Title:             US-10-600-642A-1-COPY
Perfect score:     624
Sequence:          1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 624

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 0.5

Searched:          239 seqs, 6105 residues

Total number of hits satisfying chosen parameters:       478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 239 summaries

Database :         pubnewdb:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result          Query
  No.   Score  Match Length DB  ID                       Description
----------------------------------------------------------------------------
       1    70.6   11.3    77  1  US-11-348-413-10826      Sequence 10826, A
       2    57.4    9.2    77  1  US-11-348-413-18         Sequence 18, Appl
       3    55.2    8.8    76  1  US-11-348-413-10833      Sequence 10833, A
       4  · 25      4.0    25  1  US-11-348-413-605683     Sequence 605683,
       5    25      4.0    25  1  US-11-348-413-988264     Sequence 988264,
       6    25      4.0    25  1  US-11-348-413-988265     Sequence 988265,
       7    25      4.0    25  1  US-11-348-413-988266     Sequence 988266,
       8    25      4.0    25  1  US-11-348-413-988267     Sequence 988267,
       9    25      4.0    25  1  US-11-348-413-988268     Sequence 988268,
      10    25      4.0    25  1  US-11-348-413-988269     Sequence 988269,
      11    25      4.0    25  1  US-11-348-413-988270     Sequence 988270,
      12    25      4.0    25  1  US-11-348-413-988271     Sequence 988271,
      13    25      4.0    25  1  US-11-348-413-988272     Sequence 988272,
      14    25      4.0    25  1  US-11-348-413-988273     Sequence 988273,
      15    25      4.0    25  1  US-11-348-413-988274     Sequence 988274,
      16    25      4.0    25  1  US-11-348-413-988275     Sequence 988275,
      17    25      4.0    25  1  US-11-348-413-988276     Sequence 988276,
      18    25      4.0    25  1  US-11-348-413-988277     Sequence 988277,
```

	19	25	4.0	25	1	US-11-348-413-988278	Sequence 988278,
	20	25	4.0	25	1	US-11-348-413-988279	Sequence 988279,
	21	25	4.0	25	1	US-11-348-413-988280	Sequence 988280,
	22	25	4.0	25	1	US-11-348-413-988281	Sequence 988281,
	23	25	4.0	25	1	US-11-348-413-988282	Sequence 988282,
	24	25	4.0	25	1	US-11-348-413-988283	Sequence 988283,
	25	25	4.0	25	1	US-11-348-413-988284	Sequence 988284,
	26	24	3.8	25	1	US-11-348-413-988285	Sequence 988285,
	27	23.4	3.7	25	1	US-11-348-413-605858	Sequence 605858,
	28	23.4	3.7	25	1	US-11-348-413-605859	Sequence 605859,
	29	23.4	3.7	25	1	US-11-348-413-988286	Sequence 988286,
C	30	23.4	3.7	25	1	US-11-348-413-1073654	Sequence 1073654,
C	31	23.4	3.7	25	1	US-11-348-413-1073655	Sequence 1073655,
	32	22.4	3.6	25	1	US-11-348-413-605387	Sequence 605387,
	33	22.4	3.6	25	1	US-11-348-413-605860	Sequence 605860,
	34	22.4	3.6	25	1	US-11-348-413-988811	Sequence 988811,
C	35	22	3.5	28	1	US-11-401-826-7	Sequence 7, Appli
C	36	22	3.5	28	1	US-11-255-290-7	Sequence 7, Appli
	37	21.8	3.5	25	1	US-11-348-413-605358	Sequence 605358,
	38	21.8	3.5	25	1	US-11-348-413-605359	Sequence 605359,
	39	21.8	3.5	25	1	US-11-348-413-605360	Sequence 605360,
	40	21.8	3.5	25	1	US-11-348-413-605388	Sequence 605388,
	41	21.8	3.5	25	1	US-11-348-413-605389	Sequence 605389,
	42	21.8	3.5	25	1	US-11-348-413-605390	Sequence 605390,
	43	21.8	3.5	25	1	US-11-348-413-605391	Sequence 605391,
	44	21.8	3.5	25	1	US-11-348-413-605392	Sequence 605392,
	45	21.8	3.5	25	1	US-11-348-413-605393	Sequence 605393,
	46	21.8	3.5	25	1	US-11-348-413-605394	Sequence 605394,
	47	21.8	3.5	25	1	US-11-348-413-605861	Sequence 605861,
	48	21.8	3.5	25	1	US-11-348-413-605862	Sequence 605862,
	49	21.8	3.5	25	1	US-11-348-413-605863	Sequence 605863,
	50	21.8	3.5	25	1	US-11-348-413-605864	Sequence 605864,
	51	21.8	3.5	25	1	US-11-348-413-988287	Sequence 988287,
	52	21.8	3.5	25	1	US-11-348-413-988288	Sequence 988288,
	53	21.8	3.5	25	1	US-11-348-413-988289	Sequence 988289,
	54	21.8	3.5	25	1	US-11-348-413-988290	Sequence 988290,
	55	21.8	3.5	25	1	US-11-348-413-988526	Sequence 988526,
	56	21.8	3.5	25	1	US-11-348-413-988527	Sequence 988527,
	57	21.8	3.5	25	1	US-11-348-413-988528	Sequence 988528,
	58	21.8	3.5	25	1	US-11-348-413-988812	Sequence 988812,
	59	21.8	3.5	25	1	US-11-348-413-988813	Sequence 988813,
	60	21.8	3.5	25	1	US-11-348-413-988814	Sequence 988814,
	61	21.8	3.5	25	1	US-11-348-413-988815	Sequence 988815,
	62	21.8	3.5	25	1	US-11-348-413-988816	Sequence 988816,
	63	21.8	3.5	25	1	US-11-348-413-988817	Sequence 988817,
	64	21.8	3.5	25	1	US-11-348-413-988818	Sequence 988818,
C	65	21.8	3.5	25	1	US-11-348-413-1073651	Sequence 1073651,
C	66	21.8	3.5	25	1	US-11-348-413-1073652	Sequence 1073652,
C	67	21.8	3.5	25	1	US-11-348-413-1073653	Sequence 1073653,
C	68	21.6	3.5	22	1	US-11-265-833-2	Sequence 2, Appli
C	69	21.4	3.4	25	1	US-11-348-413-1073656	Sequence 1073656,
C	70	21.2	3.4	27	1	US-11-368-333-6	Sequence 6, Appli
	71	20.8	3.3	25	1	US-11-348-413-605361	Sequence 605361,
	72	20.8	3.3	25	1	US-11-348-413-605395	Sequence 605395,
	73	20.8	3.3	25	1	US-11-348-413-605865	Sequence 605865,
	74	20.8	3.3	25	1	US-11-348-413-988291	Sequence 988291,
	75	20.8	3.3	25	1	US-11-348-413-988303	Sequence 988303,

	76	20.8	3.3	25	1	US-11-348-413-988529	Sequence 988529,
	77	20.8	3.3	25	1	US-11-348-413-988819	Sequence 988819,
	78	20.8	3.3	25	1	US-11-348-413-1222109	Sequence 1222109,
	79	20.8	3.3	25	1	US-11-348-413-1222110	Sequence 1222110,
	80	20.2	3.2	25	1	US-11-348-413-197726	Sequence 197726,
	81	20.2	3.2	25	1	US-11-348-413-557383	Sequence 557383,
	82	20.2	3.2	25	1	US-11-348-413-605362	Sequence 605362,
	83	20.2	3.2	25	1	US-11-348-413-605363	Sequence 605363,
	84	20.2	3.2	25	1	US-11-348-413-605364	Sequence 605364,
	85	20.2	3.2	25	1	US-11-348-413-605365	Sequence 605365,
	86	20.2	3.2	25	1	US-11-348-413-605366	Sequence 605366,
	87	20.2	3.2	25	1	US-11-348-413-605396	Sequence 605396,
	88	20.2	3.2	25	1	US-11-348-413-605397	Sequence 605397,
	89	20.2	3.2	25	1	US-11-348-413-605398	Sequence 605398,
	90	20.2	3.2	25	1	US-11-348-413-605399	Sequence 605399,
	91	20.2	3.2	25	1	US-11-348-413-605400	Sequence 605400,
	92	20.2	3.2	25	1	US-11-348-413-605401	Sequence 605401,
	93	20.2	3.2	25	1	US-11-348-413-605402	Sequence 605402,
	94	20.2	3.2	25	1	US-11-348-413-605866	Sequence 605866,
	95	20.2	3.2	25	1	US-11-348-413-605867	Sequence 605867,
	96	20.2	3.2	25	1	US-11-348-413-605868	Sequence 605868,
	97	20.2	3.2	25	1	US-11-348-413-605869	Sequence 605869,
	98	20.2	3.2	25	1	US-11-348-413-808694	Sequence 808694,
	99	20.2	3.2	25	1	US-11-348-413-808695	Sequence 808695,
	100	20.2	3.2	25	1	US-11-348-413-808697	Sequence 808697,
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	103	20.2	3.2	25	1	US-11-348-413-988301	Sequence 988301,
	104	20.2	3.2	25	1	US-11-348-413-988302	Sequence 988302,
	105	20.2	3.2	25	1	US-11-348-413-988530	Sequence 988530,
	106	20.2	3.2	25	1	US-11-348-413-988531	Sequence 988531,
	107	20.2	3.2	25	1	US-11-348-413-988532	Sequence 988532,
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	109	20.2	3.2	25	1	US-11-348-413-988821	Sequence 988821,
	110	20.2	3.2	25	1	US-11-348-413-988822	Sequence 988822,
	111	20.2	3.2	25	1	US-11-348-413-988823	Sequence 988823,
	112	20.2	3.2	25	1	US-11-348-413-988824	Sequence 988824,
C	113	20.2	3.2	25	1	US-11-348-413-1073649	Sequence 1073649,
C	114	20.2	3.2	25	1	US-11-348-413-1073650	Sequence 1073650,
	115	20.2	3.2	25	1	US-11-348-413-1222108	Sequence 1222108,
	116	20.2	3.2	25	1	US-11-348-413-1222134	Sequence 1222134,
	117	20.2	3.2	25	1	US-11-348-413-1222135	Sequence 1222135,
C	118	20	3.2	20	1	US-10-510-329-13	Sequence 13, Appl
C	119	20	3.2	20	1	US-11-324-675-2	Sequence 2, Appli
	120	19.8	3.2	25	1	US-11-348-413-605403	Sequence 605403,
	121	19.8	3.2	25	1	US-11-348-413-605404	Sequence 605404,
	122	19.8	3.2	25	1	US-11-348-413-808696	Sequence 808696,
	123	19.8	3.2	25	1	US-11-348-413-1222111	Sequence 1222111,
	124	19.8	3.2	25	1	US-11-348-413-1222136	Sequence 1222136,
C	125	19.4	3.1	25	1	US-11-348-413-1073657	Sequence 1073657,
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	127	19.2	3.1	25	1	US-11-348-413-605373	Sequence 605373,
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	132	19.2	3.1	25	1	US-11-348-413-808698	Sequence 808698,

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	135	19.2	3.1	25	1	US-11-348-413-988294	Sequence 988294,
	136	19.2	3.1	25	1	US-11-348-413-988300	Sequence 988300,
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	139	19.2	3.1	25	1	US-11-348-413-988540	Sequence 988540,
	140	19.2	3.1	25	1	US-11-348-413-988825	Sequence 988825,
	141	19.2	3.1	25	1	US-11-348-413-1222107	Sequence 1222107,
	142	19.2	3.1	25	1	US-11-348-413-1222138	Sequence 1222138,
C	143	19	3.0	19	1	US-11-373-989-2	Sequence 2, Appli
	144	18.8	3.0	25	1	US-11-348-413-605405	Sequence 605405,
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	146	18.8	3.0	25	1	US-11-348-413-808674	Sequence 808674,
	147	18.8	3.0	25	1	US-11-348-413-808675	Sequence 808675,
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C	149	18.8	3.0	25	1	US-11-348-413-864463	Sequence 864463,
C	150	18.8	3.0	25	1	US-11-348-413-864464	Sequence 864464,
C	151	18.8	3.0	25	1	US-11-348-413-864465	Sequence 864465,
	152	18.8	3.0	25	1	US-11-348-413-972194	Sequence 972194,
	153	18.8	3.0	25	1	US-11-348-413-1009479	Sequence 1009479,
	154	18.8	3.0	25	1	US-11-348-413-1222105	Sequence 1222105,
	155	18.8	3.0	25	1	US-11-348-413-1222106	Sequence 1222106,
	156	18.8	3.0	25	1	US-11-348-413-1222112	Sequence 1222112,
	157	18.6	3.0	25	1	US-11-348-413-605368	Sequence 605368,
	158	18.6	3.0	25	1	US-11-348-413-605369	Sequence 605369,
	159	18.6	3.0	25	1	US-11-348-413-605370	Sequence 605370,
	160	18.6	3.0	25	1	US-11-348-413-605371	Sequence 605371,
	161	18.6	3.0	25	1	US-11-348-413-605372	Sequence 605372,
	162	18.6	3.0	25	1	US-11-348-413-605406	Sequence 605406,
	163	18.6	3.0	25	1	US-11-348-413-605407	Sequence 605407,
	164	18.6	3.0	25	1	US-11-348-413-605408	Sequence 605408,
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	166	18.6	3.0	25	1	US-11-348-413-605871	Sequence 605871,
	167	18.6	3.0	25	1	US-11-348-413-605872	Sequence 605872,
	168	18.6	3.0	25	1	US-11-348-413-605873	Sequence 605873,
	169	18.6	3.0	25	1	US-11-348-413-808065	Sequence 808065,
	170	18.6	3.0	25	1	US-11-348-413-808066	Sequence 808066,
	171	18.6	3.0	25	1	US-11-348-413-808067	Sequence 808067,
	172	18.6	3.0	25	1	US-11-348-413-808068	Sequence 808068,
	173	18.6	3.0	25	1	US-11-348-413-808701	Sequence 808701,
	174	18.6	3.0	25	1	US-11-348-413-808702	Sequence 808702,
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C	176	18.6	3.0	25	1	US-11-348-413-864461	Sequence 864461,
C	177	18.6	3.0	25	1	US-11-348-413-864466	Sequence 864466,
	178	18.6	3.0	25	1	US-11-348-413-988295	Sequence 988295,
	179	18.6	3.0	25	1	US-11-348-413-988296	Sequence 988296,
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	181	18.6	3.0	25	1	US-11-348-413-988298	Sequence 988298,
	182	18.6	3.0	25	1	US-11-348-413-988299	Sequence 988299,
	183	18.6	3.0	25	1	US-11-348-413-988489	Sequence 988489,
	184	18.6	3.0	25	1	US-11-348-413-988534	Sequence 988534,
	185	18.6	3.0	25	1	US-11-348-413-988535	Sequence 988535,
	186	18.6	3.0	25	1	US-11-348-413-988536	Sequence 988536,
	187	18.6	3.0	25	1	US-11-348-413-988537	Sequence 988537,
	188	18.6	3.0	25	1	US-11-348-413-988538	Sequence 988538,
	189	18.6	3.0	25	1	US-11-348-413-988826	Sequence 988826,

190	18.6	3.0	25	1	US-11-348-413-1064914	Sequence 1064914,
c 191	18.6	3.0	25	1	US-11-348-413-1165354	Sequence 1165354,
192	18.6	3.0	25	1	US-11-348-413-1210461	Sequence 1210461,
193	18.6	3.0	25	1	US-11-348-413-1210462	Sequence 1210462,
194	18.6	3.0	25	1	US-11-348-413-1222137	Sequence 1222137,
195	18.6	3.0	25	1	US-11-348-413-1222139	Sequence 1222139,
196	18.6	3.0	25	1	US-11-348-413-1222140	Sequence 1222140,
197	18.4	2.9	25	1	US-11-348-413-808064	Sequence 808064,
c 198	18.4	2.9	25	1	US-11-348-413-864462	Sequence 864462,
199	18.2	2.9	25	1	US-11-217-529-118810	Sequence 118810,
c 200	18.2	2.9	25	1	US-11-348-413-202363	Sequence 202363,
201	18.2	2.9	25	1	US-11-348-413-605375	Sequence 605375,
202	18.2	2.9	25	1	US-11-348-413-808679	Sequence 808679,
203	18.2	2.9	25	1	US-11-348-413-988541	Sequence 988541,
204	18.2	2.9	25	1	US-11-348-413-988827	Sequence 988827,
205	18.2	2.9	25	1	US-11-348-413-988828	Sequence 988828,
206	18.2	2.9	25	1	US-11-348-413-1055941	Sequence 1055941,
c 207	18.2	2.9	25	1	US-11-348-413-1073648	Sequence 1073648,
c 208	18	2.9	18	1	US-11-350-955-9	Sequence 9, Appli
c 209	18	2.9	18	1	US-11-350-796-9	Sequence 9, Appli
210	17.8	2.9	25	1	US-11-348-413-797854	Sequence 797854,
c 211	17.8	2.9	25	1	US-11-348-413-804342	Sequence 804342,
212	17.8	2.9	25	1	US-11-348-413-808672	Sequence 808672,
c 213	17.8	2.9	25	1	US-11-348-413-1009551	Sequence 1009551,
214	17.8	2.9	25	1	US-11-348-413-1222104	Sequence 1222104,
215	17.8	2.9	25	1	US-11-348-413-1222113	Sequence 1222113,
c 216	17.6	2.8	25	1	US-11-348-413-222739	Sequence 222739,
217	17.6	2.8	25	1	US-11-348-413-350696	Sequence 350696,
218	17.6	2.8	25	1	US-11-348-413-434686	Sequence 434686,
219	17.6	2.8	25	1	US-11-348-413-434687	Sequence 434687,
220	17.6	2.8	25	1	US-11-348-413-572608	Sequence 572608,
221	17.6	2.8	25	1	US-11-348-413-605379	Sequence 605379,
222	17.6	2.8	25	1	US-11-348-413-605380	Sequence 605380,
223	17.6	2.8	25	1	US-11-348-413-605409	Sequence 605409,
224	17.6	2.8	25	1	US-11-348-413-605874	Sequence 605874,
225	17.6	2.8	25	1	US-11-348-413-808069	Sequence 808069,
226	17.6	2.8	25	1	US-11-348-413-808703	Sequence 808703,
227	17.6	2.8	25	1	US-11-348-413-808707	Sequence 808707,
228	17.6	2.8	25	1	US-11-348-413-808708	Sequence 808708,
c 229	17.6	2.8	25	1	US-11-348-413-864459	Sequence 864459,
c 230	17.6	2.8	25	1	US-11-348-413-864467	Sequence 864467,
c 231	17.6	2.8	25	1	US-11-348-413-900967	Sequence 900967,
232	17.6	2.8	25	1	US-11-348-413-930121	Sequence 930121,
233	17.6	2.8	25	1	US-11-348-413-988488	Sequence 988488,
234	17.6	2.8	25	1	US-11-348-413-988490	Sequence 988490,
235	17.6	2.8	25	1	US-11-348-413-988545	Sequence 988545,
236	17.6	2.8	25	1	US-11-348-413-988546	Sequence 988546,
237	17.6	2.8	25	1	US-11-348-413-1075989	Sequence 1075989,
238	17.6	2.8	25	1	US-11-348-413-1222141	Sequence 1222141,
239	17.6	2.8	25	1	US-11-348-413-1238534	Sequence 1238534,

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:27:10 ; Search time 0.001 Seconds
                                            (without alignments)
                                            896.376 Million cell updates/sec

Title: US-10-600-642A-2-COPY
Perfect score: 442
Sequence: 1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 442

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 24 seqs, 1014 residues

Total number of hits satisfying chosen parameters: 48

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 24 summaries

Database :   pubmaindb2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                          %
Result   Query
    No.   Score   Match Length DB   ID   Description
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        1   442 100.0   442 1   US-10-600-642-2   Sequence 2, Appli
        2   26.8   6.1   30 1   US-10-881-813-4   Sequence 4, Appli
        3   26   5.9   35 1   US-10-223-126-202   Sequence 202, App
        4   26   5.9   35 1   US-11-070-519-202   Sequence 202, App
        5   25.2   5.7   30 1   US-10-831-286A-16801   Sequence 16801, A
        6   25   5.7   25 1   US-10-401-343-42   Sequence 42, Appl
        7   25   5.7   25 1   US-11-237-807-42   Sequence 42, Appl
        8   23.6   5.3   30 1   US-09-807-723-1   Sequence 1, Appli
        9   23.6   5.3   30 1   US-10-770-183-1   Sequence 1, Appli
  C   10   22   5.0   22 1   US-09-991-518A-2   Sequence 2, Appli
  C   11   22   5.0   22 1   US-10-810-550-110   Sequence 110, App
  C   12   22   5.0   22 1   US-10-805-292-76   Sequence 76, Appl
  C   13   22   5.0   22 1   US-10-972-530-10   Sequence 10, Appl
  C   14   22   5.0   22 1   US-10-848-126-76   Sequence 76, Appl
  C   15   22   5.0   22 1   US-11-228-416-2   Sequence 2, Appli
  C   16   21.6   4.9   22 1   US-10-396-446-5   Sequence 5, Appli
  C   17   21.6   4.9   22 1   US-10-477-469-10   Sequence 10, Appl

c	18	21.6	4.9	22	1	US-11-273-617-13	Sequence 13, Appl
	19	21.4	4.8	23	1	US-10-360-935-37	Sequence 37, Appl
c	20	21.2	4.8	27	1	US-10-407-952-6	Sequence 6, Appli
	21	21	4.8	21	1	US-10-438-774-5	Sequence 5, Appli
c	22	20.6	4.7	21	1	US-10-212-476-4	Sequence 4, Appli
c	23	20.6	4.7	21	1	US-10-466-016-2	Sequence 2, Appli
c	24	20.6	4.7	21	1	US-10-793-643A-2	Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:04:59 ; Search time 0.001 Seconds
                                             (without alignments)
                                             2875.392 Million cell updates/sec

Title: US-10-600-642A-1-COPY
Perfect score: 624
Sequence: 1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 624

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 22 seqs, 2304 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 22 summaries

Database :   pubmaindb:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
               %
Result   Query
  No. Score Match Length DB ID   Description
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    2 337.8 54.1   442 1 US-10-600-642-2   Sequence 2, Appli
    3   69 11.1   77 1 US-09-974-300-8397   Sequence 8397, Ap
    4   69 11.1   77 1 US-09-974-300-8406   Sequence 8406, Ap
    5   69 11.1   77 1 US-09-974-300-8454   Sequence 8454, Ap
    6   67.6 10.8   74 1 US-10-857-625-228   Sequence 228, App
    7   67.6 10.8   74 1 US-10-857-625-388   Sequence 388, App
    8   67.4 10.8   77 1 US-09-974-300-4362   Sequence 4362, Ap
    9   67.4 10.8   77 1 US-09-974-300-4371   Sequence 4371, Ap
   10   67.4 10.8   77 1 US-09-974-300-4377   Sequence 4377, Ap
   11   67.4 10.8   77 1 US-09-974-300-4419   Sequence 4419, Ap
   12   66.4 10.6   76 1 US-09-974-300-4375   Sequence 4375, Ap
   13   66.4 10.6   76 1 US-09-974-300-4436   Sequence 4436, Ap
   14   52.2   8.4   73 1 US-10-857-625-226   Sequence 226, App
   15   52.2   8.4   73 1 US-10-857-625-389   Sequence 389, App
   16   52.2   8.4   73 1 US-10-857-625-400   Sequence 400, App
   17   26.8   4.3   30 1 US-10-881-813-4   Sequence 4, Appli

18	26	4.2	35	1	US-10-223-126-202	Sequence 202, App
19	26	4.2	35	1	US-11-070-519-202	Sequence 202, App
20	25.2	4.0	30	1	US-10-831-286A-16801	Sequence 16801, A
21	25	4.0	25	1	US-10-401-343-42	Sequence 42, Appl
22	25	4.0	25	1	US-11-237-807-42	Sequence 42, Appl

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OM nucleic - nucleic search, using sw model

Run on:          August 18, 2006, 15:07:10 ; Search time 0.001 Seconds
                                             (without alignments)
                                             5257.824 Million cell updates/sec

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Perfect score:  624
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched:       22 seqs, 4213 residues

Total number of hits satisfying chosen parameters:      44

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 22 summaries

Database :      gedb:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                               SUMMARIES
                   %
Result          Query
  No.   Score  Match Length DB  ID              Description
--------------------------------------------------------------------------------
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     2    624  100.0    624   1  AR408838        ACCESSION:AR408838
     3    624  100.0    624   1  AB022063        ACCESSION:AB022063
     4  337.8   54.1    442   1  E54412          ACCESSION:E54412
     5  337.8   54.1    442   1  AR408839        ACCESSION:AR408839
     6  337.8   54.1    442   1  AB022064        ACCESSION:AB022064
     7     69   11.1     77   1  AX439982        ACCESSION:AX439982
     8     69   11.1     77   1  AX439991        ACCESSION:AX439991
     9     69   11.1     77   1  AX440039        ACCESSION:AX440039
    10   67.4   10.8     77   1  AX435947        ACCESSION:AX435947
    11   67.4   10.8     77   1  AX435956        ACCESSION:AX435956
    12   67.4   10.8     77   1  AX435962        ACCESSION:AX435962
    13   67.4   10.8     77   1  AX436004        ACCESSION:AX436004
    14   66.4   10.6     76   1  AX435960        ACCESSION:AX435960
    15   66.4   10.6     76   1  AX436021        ACCESSION:AX436021
    16     60    9.6     77   1  ECOTRI1         ACCESSION:K00217
    17   50.4    8.1     52   1  BACRRDA         ACCESSION:M13610
    18   48.2    7.7     61   1  AB201400        ACCESSION:AB201400
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   19    45.2    7.2     50  1  STMRR16S          ACCESSION:M26120
   20    26.8    4.3     30  1  CS001459          ACCESSION:CS001459
C  21    23.8    3.8     27  1  AR124123          ACCESSION:AR124123
C  22    23.8    3.8     27  1  AR282388          ACCESSION:AR282388
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:02:08 ; Search time 1 Seconds
                                           (without alignments)
                                           2.621 Million cell updates/sec

Title: US-10-600-642A-1-COPY
Perfect score: 624
Sequence: 1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 624

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched: 27 seqs, 2100 residues

Total number of hits satisfying chosen parameters: 54

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

score/length
seq 1

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 27 summaries

Database :   issdb:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
    No.   Score Match Length DB   ID   Description
    ----
       1   624 100.0   624 1   US-09-762-633-1   Sequence 1, Appli
       2   337.8   54.1   442 1   US-09-762-633-2   Sequence 2, Appli
       3   69   11.1   77 1   US-09-974-300-8397   Sequence 8397, Ap
       4   69   11.1   77 1   US-09-974-300-8406   Sequence 8406, Ap
       5   69   11.1   77 1   US-09-974-300-8454   Sequence 8454, Ap
       6   67.4   10.8   77 1   US-09-974-300-4362   Sequence 4362, Ap
       7   67.4   10.8   77 1   US-09-974-300-4371   Sequence 4371, Ap
       8   67.4   10.8   77 1   US-09-974-300-4377   Sequence 4377, Ap
       9   67.4   10.8   77 1   US-09-974-300-4419   Sequence 4419, Ap
      10   66.4   10.6   76 1   US-09-974-300-4375   Sequence 4375, Ap
      11   66.4   10.6   76 1   US-09-974-300-4436   Sequence 4436, Ap
  c   12   23.8   3.8   27 1   US-09-252-806-2   Sequence 2, Appli
  c   13   23.8   3.8   27 1   US-09-711-508-2   Sequence 2, Appli
  c   14   21.6   3.5   22 1   US-08-995-960-18   Sequence 18, Appl
  c   15   21.6   3.5   22 1   US-08-953-171-39   Sequence 39, Appl
  c   16   21.6   3.5   22 1   US-09-193-377B-61   Sequence 61, Appl
  c   17   20.6   3.3   21 1   US-08-266-414-3   Sequence 3, Appli

c	18	20.6	3.3	21	1	US-08-953-171-22	Sequence 22, Appl
c	19	20.6	3.3	21	1	US-09-261-115-4	Sequence 4, Appli
	20	20	3.2	20	1	US-08-445-289B-9	Sequence 9, Appli
c	21	20	3.2	20	1	US-09-073-465-17	Sequence 17, Appl
	22	20	3.2	20	1	US-09-398-179-5	Sequence 5, Appli
c	23	20	3.2	20	1	US-09-883-405-2	Sequence 2, Appli
c	24	20	3.2	20	1	US-10-085-871C-8	Sequence 8, Appli
c	25	20	3.2	20	1	US-10-085-871C-12	Sequence 12, Appl
c	26	20	3.2	20	1	US-09-856-221-5	Sequence 5, Appli
c	27	20	3.2	20	1	US-10-166-225A-3	Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:03:40 ; Search time 0.001 Seconds
                                            (without alignments)
                                            5683.392 Million cell updates/sec

Title: US-10-600-642A-1-COPY
Perfect score: 624
Sequence: 1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 624

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 74 seqs, 4554 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 74 summaries

Database :   ngsdb:*

score/length genesca/ SID1 (handwritten)

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
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     1   624 100.0   624 1   AAZ91771   Spacer region betw
     2   624 100.0   624 1   AAI71855   Pectinatus frising
     3   337.8   54.1   442 1   AAZ91772   Spacer region betw
     4   337.8   54.1   442 1   AAI71856   Pectinatus frising
     5   69   11.1   77 1   ABK81163   Bacillus clausii g
     6   69   11.1   77 1   ABK81115   Bacillus clausii g
     7   69   11.1   77 1   ABK81106   Bacillus clausii g
     8   67.6   10.8   74 1   ADW94448   Proliferation-requ
     9   67.6   10.8   74 1   ADW94288   Proliferation-requ
    10   67.4   10.8   77 1   ABK77071   Bacillus lichenifo
    11   67.4   10.8   77 1   ABK77080   Bacillus lichenifo
    12   67.4   10.8   77 1   ABK77128   Bacillus lichenifo
    13   67.4   10.8   77 1   ABK77086   Bacillus lichenifo
    14   66.4   10.6   76 1   ABK77145   Bacillus lichenifo
    15   66.4   10.6   76 1   ABK77084   Bacillus lichenifo
    16   52.2   8.4   73 1   ADW94460   Proliferation-requ
    17   52.2   8.4   73 1   ADW94286   Proliferation-requ
    18   52.2   8.4   73 1   ADW94449   Proliferation-requ

	19	30.4	4.9	41	1	ADB61527	Prokaryotic gene s
	20	29.8	4.8	40	1	AEC64592	Organochlorine com
	21	28.8	4.6	40	1	AEC64617	Organochlorine com
	22	28.8	4.6	40	1	AEC64616	Organochlorine com
	23	26.8	4.3	30	1	ADX17032	Lemna minor chloro
c	24	26	4.2	26	1	AAQ92375	DNA primer. Synth
	25	26	4.2	35	1	ACC97191	Consensus 16S rRNA
	26	25	4.0	25	1	ADF69484	Tapesia acuformisI
c	27	23.8	3.8	27	1	AAX04478	Strain MO7 16S rDN
c	28	23.6	3.8	30	1	AAQ71864	Eucaryotic nuclear
	29	23.6	3.8	30	1	AAI64203	Primer 1P for the
c	30	23.4	3.7	25	1	AAQ44665	Primer #1 for PCR/
c	31	22.2	3.6	27	1	AAV21874	Antisense oligo NB
c	32	22.2	3.6	27	1	AAV17792	Microorganism MO7
c	33	22	3.5	22	1	AAX04638	PCR primer 2 used
c	34	22	3.5	22	1	AAZ09417	E. coli 16S rRNA s
	35	22	3.5	22	1	AAK99084	S. aureus 16S-rRNA
c	36	22	3.5	22	1	ABN84205	Salinospora sp. 16
	37	22	3.5	22	1	AAK99123	Staphylococcus aur
c	38	22	3.5	22	1	ADS18913	Reverse PCR primer
c	39	22	3.5	22	1	ADU40707	Novel nucleotide a
c	40	22	3.5	22	1	ADZ66121	16s rRNA reverse P
c	41	22	3.5	22	1	ADU76905	16s rRNA reverse P
c	42	22	3.5	22	1	ADZ69178	Eubacterial PCR pr
c	43	22	3.5	22	1	AEC81382	Dehalococcoides ba
c	44	22	3.5	22	1	AEF24204	rRNA SSU primer RC
c	45	21.6	3.5	22	1	AAX82007	Bacterial 16S rRNA
c	46	21.6	3.5	22	1	AAZ86877	16S rRNA PCR prime
c	47	21.6	3.5	22	1	AAF54840	Primer used for sp
c	48	21.6	3.5	22	1	ABZ69287	J lividum 16s ribo
c	49	21.6	3.5	22	1	ABZ23953	A. radiobacter 16S
c	50	21.6	3.5	22	1	ADG25781	Bacterial universa
c	51	21.6	3.5	22	1	ADK65756	Reverse primer 149
c	52	21.6	3.5	22	1	ADU39844	Alcanivorax sp. OK
c	53	21.6	3.5	22	1	ADV25289	Primer 1492R used
c	54	21.6	3.5	22	1	ADW16281	PCR primer 1492r t
	55	21.4	3.4	23	1	ADS17007	Primer used to det
c	56	21.2	3.4	27	1	ADE85928	Escherichia coli 1
c	57	21	3.4	21	1	AAQ10127	Probe 1640 to the
c	58	21	3.4	21	1	AAT11573	16S rRNA reverse p
c	59	21	3.4	21	1	AAV21120	16S rRNA Escherich
	60	21	3.4	21	1	AAH73860	Cyanophycean PCR p
c	61	21	3.4	21	1	ACC48610	Erwinia pyrifoliae
c	62	21	3.4	21	1	ADL15738	Bacillus CMB26 str
c	63	21	3.4	21	1	ADS75285	Universal PCR prim
c	64	21	3.4	21	1	AEC09675	Primer 16S-2, seq
c	65	21	3.4	21	1	AEE19758	Pseudomonas chloro
c	66	21	3.4	21	1	AEE75252	Acinetobacter sp.
	67	21	3.4	24	1	AAI69778	16S/23SrRNA spacer
c	68	20.6	3.3	21	1	AAT60344	Reverse primer for
c	69	20.6	3.3	21	1	AAV45917	Biosensor oligonuc
c	70	20.6	3.3	21	1	AAX57749	Oligonucleotide 14
c	71	20.6	3.3	21	1	AAC58781	Bacterial 16S rRNA
c	72	20.6	3.3	21	1	ABS53672	Antimicrobial agen
c	73	20.6	3.3	21	1	ADV96672	Rhizobium 16S rDNA
c	74	20.6	3.3	27	1	AAV21876	Nuclease resistant

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:25:09 ; Search time 0.001 Seconds
                                            (without alignments)
                                            2085.356 Million cell updates/sec

Title: US-10-600-642A-2-COPY
Perfect score: 442
Sequence: 1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 442

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 100 seqs, 2359 residues

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 101 summaries

Database :   issdb2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
    No.   Score Match Length DB ID   Description
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        1   442 100.0   442 1 US-09-762-633-2   Sequence 2, Appli
  c   2   23.8   5.4   27 1 US-09-252-806-2   Sequence 2, Appli
  c   3   23.8   5.4   27 1 US-09-711-508-2   Sequence 2, Appli
  c   4   21.6   4.9   22 1 US-08-995-960-18   Sequence 18, Appl
  c   5   21.6   4.9   22 1 US-08-953-171-39   Sequence 39, Appl
  c   6   21.6   4.9   22 1 US-09-193-377B-61   Sequence 61, Appl
  c   7   20.6   4.7   21 1 US-08-266-414-3   Sequence 3, Appli
  c   8   20.6   4.7   21 1 US-08-953-171-22   Sequence 22, Appl
  c   9   20.6   4.7   21 1 US-09-261-115-4   Sequence 4, Appli
       10   20   4.5   20 1 US-08-445-289B-9   Sequence 9, Appli
  c   11   20   4.5   20 1 US-09-073-465-17   Sequence 17, Appl
       12   20   4.5   20 1 US-09-398-179-5   Sequence 5, Appli
  c   13   20   4.5   20 1 US-09-883-405-2   Sequence 2, Appli
  c   14   20   4.5   20 1 US-10-085-871C-8   Sequence 8, Appli
  c   15   20   4.5   20 1 US-10-085-871C-12   Sequence 12, Appl
  c   16   20   4.5   20 1 US-09-856-221-5   Sequence 5, Appli
  c   17   20   4.5   20 1 US-10-166-225A-3   Sequence 3, Appli
  c   18   19   4.3   19 1 US-09-924-097A-17   Sequence 17, Appl

c	19	19	4.3	19	1	US-09-762-633-5	Sequence 5, Appli
c	20	19	4.3	19	1	US-10-069-977-2	Sequence 2, Appli
c	21	19	4.3	19	1	US-10-069-977-5	Sequence 5, Appli
c	22	19	4.3	442	1	US-09-762-633-2	Sequence 2, Appli
c	23	18.6	4.2	19	1	US-09-557-248-4	Sequence 4, Appli
c	24	18.6	4.2	20	1	US-10-053-243-9	Sequence 9, Appli
	25	18.4	4.2	20	1	US-08-445-289B-7	Sequence 7, Appli
	26	18.4	4.2	20	1	US-08-445-289B-10	Sequence 10, Appl
c	27	18.4	4.2	20	1	US-09-073-465-16	Sequence 16, Appl
c	28	18.4	4.2	20	1	US-09-762-633-6	Sequence 6, Appli
c	29	18	4.1	19	1	US-09-998-551E-2	Sequence 2, Appli
c	30	17.4	3.9	19	1	US-07-971-819A-15	Sequence 15, Appl
c	31	17.4	3.9	19	1	US-08-384-490-29	Sequence 29, Appl
c	32	17.4	3.9	19	1	US-08-244-269-26	Sequence 26, Appl
c	33	17.4	3.9	19	1	US-08-475-231-15	Sequence 15, Appl
c	34	17.4	3.9	19	1	US-08-348-683-1	Sequence 1, Appli
c	35	17.4	3.9	19	1	US-08-459-383-29	Sequence 29, Appl
c	36	17.4	3.9	19	1	US-08-665-565B-2	Sequence 2, Appli
c	37	17.4	3.9	19	1	US-08-665-565B-4	Sequence 4, Appli
c	38	17.4	3.9	19	1	US-09-034-724-2	Sequence 2, Appli
c	39	17.4	3.9	19	1	US-09-034-724-4	Sequence 4, Appli
c	40	17.4	3.9	19	1	US-09-191-099-10	Sequence 10, Appl
c	41	17.4	3.9	19	1	US-09-216-909-5	Sequence 5, Appli
c	42	17.4	3.9	19	1	US-09-311-260-166	Sequence 166, App
c	43	17.4	3.9	19	1	US-09-702-843-5	Sequence 5, Appli
c	44	17.4	3.9	19	1	US-09-702-847-5	Sequence 5, Appli
c	45	17.4	3.9	19	1	US-08-943-571-4	Sequence 4, Appli
c	46	17.4	3.9	19	1	US-09-549-853-6	Sequence 6, Appli
c	47	17.4	3.9	19	1	US-09-437-905-2	Sequence 2, Appli
c	48	17.4	3.9	19	1	US-09-437-905-4	Sequence 4, Appli
c	49	17.4	3.9	19	1	US-09-848-083-2	Sequence 2, Appli
c	50	17.4	3.9	19	1	US-09-714-780-4	Sequence 4, Appli
c	51	17.4	3.9	19	1	US-09-687-219-2	Sequence 2, Appli
c	52	17.4	3.9	19	1	US-09-848-651-2	Sequence 2, Appli
c	53	17.4	3.9	19	1	US-09-848-095-2	Sequence 2, Appli
c	54	17.4	3.9	19	1	US-10-272-490-94	Sequence 94, Appl
c	55	17.4	3.9	19	1	US-10-053-243-8	Sequence 8, Appli
c	56	17.4	3.9	19	1	US-09-444-112-2	Sequence 2, Appli
c	57	17.4	3.9	19	1	US-10-214-473-83	Sequence 83, Appl
c	58	17.4	3.9	19	1	US-09-663-620-4	Sequence 4, Appli
c	59	17.2	3.9	23	1	US-09-335-231-4	Sequence 4, Appli
	60	17	3.8	17	1	US-08-144-212-18	Sequence 18, Appl
c	61	17	3.8	17	1	US-07-744-282C-118	Sequence 118, App
c	62	17	3.8	17	1	PCT-US92-06821A-124	Sequence 124, App
	63	17	3.8	22	1	US-08-412-614-101	Sequence 101, App
	64	17	3.8	22	1	US-08-412-614-103	Sequence 103, App
	65	17	3.8	22	1	US-08-635-761-101	Sequence 101, App
	66	17	3.8	22	1	US-08-635-761-103	Sequence 103, App
c	67	17	3.8	22	1	US-09-066-046-41	Sequence 41, Appl
	68	17	3.8	22	1	US-09-312-520-101	Sequence 101, App
	69	17	3.8	22	1	US-09-312-520-103	Sequence 103, App
	70	17	3.8	22	1	US-09-863-086-101	Sequence 101, App
	71	17	3.8	22	1	US-09-863-086-103	Sequence 103, App
c	72	17	3.8	23	1	US-08-778-217-8	Sequence 8, Appli
c	73	17	3.8	23	1	US-08-821-948-8	Sequence 8, Appli
	74	17	3.8	23	1	US-08-765-332-155	Sequence 155, App
	75	17	3.8	23	1	US-09-448-894-155	Sequence 155, App

c	76	17	3.8	23	1	US-09-397-955C-8	Sequence 8, Appli
	77	17	3.8	23	1	US-09-931-486-155	Sequence 155, App
	78	16.8	3.8	20	1	US-08-445-289B-8	Sequence 8, Appli
c	79	16.4	3.7	18	1	US-10-069-977-3	Sequence 3, Appli
c	80	16.4	3.7	18	1	US-09-786-253-9	Sequence 9, Appli
c	81	16.2	3.7	17	1	US-08-733-816-2	Sequence 2, Appli
c	82	16.2	3.7	17	1	US-08-892-540-2	Sequence 2, Appli
c	83	16.2	3.7	17	1	US-08-953-171-40	Sequence 40, Appl
c	84	16	3.6	16	1	US-09-342-579-3	Sequence 3, Appli
	85	16	3.6	16	1	US-09-398-179-17	Sequence 17, Appl
c	86	16	3.6	16	1	US-09-504-358-34	Sequence 34, Appl
c	87	16	3.6	16	1	US-09-617-854A-3	Sequence 3, Appli
c	88	16	3.6	16	1	US-09-954-314-34	Sequence 34, Appl
c	89	16	3.6	16	1	US-09-648-004-29	Sequence 29, Appl
c	90	16	3.6	16	1	US-09-716-865-25	Sequence 25, Appl
c	91	16	3.6	16	1	US-09-735-567-9	Sequence 9, Appli
c	92	16	3.6	16	1	US-10-230-562-34	Sequence 34, Appl
c	93	16	3.6	16	1	US-10-272-419-29	Sequence 29, Appl
c	94	16	3.6	16	1	US-10-007-527A-10	Sequence 10, Appl
c	95	16	3.6	16	1	US-09-941-947A-46	Sequence 46, Appl
c	96	16	3.6	16	1	US-10-209-372-24	Sequence 24, Appl
c	97	16	3.6	16	1	US-10-128-713A-22	Sequence 22, Appl
	98	16	3.6	17	1	US-08-242-664-34	Sequence 34, Appl
	99	16	3.6	17	1	US-08-484-138-34	Sequence 34, Appl
	100	16	3.6	17	1	US-09-052-333A-47	Sequence 47, Appl
	101	16	3.6	17	1	PCT-US95-06379-34	Sequence 34, Appl

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       GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:            August 18, 2006, 15:26:20 ; Search time 1 Seconds
                                               (without alignments)
                                               3.446 Million cell updates/sec

Title:             US-10-600-642A-2-COPY
Perfect score:     442
Sequence:          1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 442

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 0.5

Searched:          142 seqs, 3898 residues

Total number of hits satisfying chosen parameters:       284

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 142 summaries

Database :         ngsdb2:*
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Score/length Seq 2

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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result              Query
    No.    Score   Match Length DB   ID                  Description
    ------------------------------------------------------------------------
       1     442   100.0    442  1   AAZ91772            Spacer region betw
       2     442   100.0    442  1   AAI71856            Pectinatus frising
       3    30.4     6.9     41  1   ADB61527            Prokaryotic gene s
       4    29.8     6.7     40  1   AEC64592            Organochlorine com
       5    26.8     6.1     30  1   ADX17032            Lemna minor chloro
  c    6      26     5.9     26  1   AAQ92375            DNA primer.  Synth
       7      26     5.9     35  1   ACC97191            Consensus 16S rRNA
       8      25     5.7     25  1   ADF69484            Tapesia acuformisI
  c    9    23.8     5.4     27  1   AAX04478            Strain MO7 16S rDN
  c   10    23.6     5.3     30  1   AAQ71864            Eucaryotic nuclear
      11    23.6     5.3     30  1   AAI64203            Primer 1P for the
  c   12    23.4     5.3     25  1   AAQ44665            Primer #1 for PCR/
  c   13    22.2     5.0     27  1   AAV17792            Microorganism MO7
  c   14      22     5.0     22  1   AAX04638            PCR primer 2 used
  c   15      22     5.0     22  1   AAZ09417            E. coli 16S rRNA s
      16      22     5.0     22  1   AAK99084            S. aureus 16S-rRNA
  c   17      22     5.0     22  1   ABN84205            Salinospora sp. 16
      18      22     5.0     22  1   AAK99123            Staphylococcus aur
```

c	19	22	5.0	22	1	ADS18913	Reverse PCR primer
c	20	22	5.0	22	1	ADU40707	Novel nucleotide a
c	21	22	5.0	22	1	ADZ66121	16s rRNA reverse P
c	22	22	5.0	22	1	ADU76905	16s rRNA reverse P
c	23	22	5.0	22	1	ADZ69178	Eubacterial PCR pr
c	24	22	5.0	22	1	AEC81382	Dehalococcoides ba
c	25	22	5.0	22	1	AEF24204	rRNA SSU primer RC
c	26	21.6	4.9	22	1	AAX82007	Bacterial 16S rRNA
c	27	21.6	4.9	22	1	AAZ86877	16S rRNA PCR prime
c	28	21.6	4.9	22	1	AAF54840	Primer used for sp
c	29	21.6	4.9	22	1	ABZ69287	J lividum 16s ribo
c	30	21.6	4.9	22	1	ABZ23953	A. radiobacter 16S
c	31	21.6	4.9	22	1	ADG25781	Bacterial universa
c	32	21.6	4.9	22	1	ADK65756	Reverse primer 149
c	33	21.6	4.9	22	1	ADU39844	Alcanivorax sp. OK
c	34	21.6	4.9	22	1	ADV25289	Primer 1492R used
c	35	21.6	4.9	22	1	ADW16281	PCR primer 1492r t
	36	21.4	4.8	23	1	ADS17007	Primer used to det
c	37	21.2	4.8	27	1	ADE85928	Escherichia coli 1
c	38	21	4.8	21	1	AAQ10127	Probe 1640 to the
c	39	21	4.8	21	1	AAT11573	16S rRNA reverse p
c	40	21	4.8	21	1	AAV21120	16S rRNA Escherich
	41	21	4.8	21	1	AAH73860	Cyanophycean PCR p
c	42	21	4.8	21	1	ACC48610	Erwinia pyrifoliae
c	43	21	4.8	21	1	ADL15738	Bacillus CMB26 str
c	44	21	4.8	21	1	ADS75285	Universal PCR prim
c	45	21	4.8	21	1	AEC09675	Primer 16S-2, seq
c	46	21	4.8	21	1	AEE19758	Pseudomonas chloro
c	47	21	4.8	21	1	AEE75252	Acinetobacter sp.
	48	21	4.8	24	1	AAI69778	16S/23SrRNA spacer
c	49	20.6	4.7	21	1	AAT60344	Reverse primer for
c	50	20.6	4.7	21	1	AAV45917	Biosensor oligonuc
c	51	20.6	4.7	21	1	AAX57749	Oligonucleotide 14
c	52	20.6	4.7	21	1	AAC58781	Bacterial 16S rRNA
c	53	20.6	4.7	21	1	ABS53672	Antimicrobial agen
c	54	20.6	4.7	21	1	ADV96672	Rhizobium 16S rDNA
	55	20.4	4.6	22	1	ABQ78789	PCR primer Eub1492
c	56	20.4	4.6	22	1	ADF17490	Pseudomonas putida
c	57	20.4	4.6	22	1	ADW16284	PCR primer 1492r t
c	58	20.4	4.6	22	1	AEC37152	H. variabilis 16S
c	59	20	4.5	20	1	AAQ54377	LAB rRNA gene prim
	60	20	4.5	20	1	AAQ65326	PCR primer R16-2 t
	61	20	4.5	20	1	AAQ62069	Lactobacillus 16S/
	62	20	4.5	20	1	AAQ88202	Lactobacillus sp.
	63	20	4.5	20	1	AAT45337	Mycoplasma second
	64	20	4.5	20	1	AAA08717	Bartonella genus s
c	65	20	4.5	20	1	AAA39039	Unknown bacterial
c	66	20	4.5	20	1	AAH73455	Brevibacillus bors
c	67	20	4.5	20	1	AAF95144	rrs gene PCR prime
c	68	20	4.5	20	1	AAH26928	Brevibacillus bors
c	69	20	4.5	20	1	ABQ75101	16S rDNA PCR prime
c	70	20	4.5	20	1	ACA99381	Enzyme DNA PCR pri
c	71	20	4.5	20	1	ADD29134	Nitrification bact
	72	20	4.5	20	1	ADK70934	Cff DNA related PC
c	73	20	4.5	20	1	ADF56681	Saccharothrix sp 1
c	74	20	4.5	20	1	ADG64526	PCR primer GMG 6 #
c	75	20	4.5	20	1	ADG64530	PCR primer GMG 9 #

c	76	20	4.5	20	1	ADQ78389	16S rRNA related p
c	77	20	4.5	20	1	ADQ67901	PCR primer BSR IS4
c	78	20	4.5	20	1	ADQ67897	PCR primer BSR IS4
c	79	20	4.5	20	1	ADQ74959	Sphingomonas sp. K
c	80	20	4.5	20	1	ADS15244	H.pylori 16s rRNA
c	81	20	4.5	20	1	ADS15215	Primer used in 16s
c	82	20	4.5	20	1	ADU39842	Acinetobacter sp.
c	83	20	4.5	20	1	ADW43199	Universal bacteria
c	84	20	4.5	20	1	ADY86154	16s rDNA amplifyin
c	85	20	4.5	20	1	ADY86158	16s rDNA amplifyin
c	86	20	4.5	20	1	ADZ99827	Primer used to amp
c	87	20	4.5	20	1	AED29539	Bacillus sp. 16S r
c	88	20	4.5	20	1	AED67223	Microbe WatG 16S r
c	89	20	4.5	20	1	AEE97981	16S rDNA gene PCR
c	90	20	4.5	20	1	AEE98064	16S rDNA gene PCR
c	91	20	4.5	22	1	ADS16972	16s and 18s rDNA g
	92	20	4.5	25	1	ADX82366	Lactobacillus forw
	93	19.8	4.5	23	1	AAA14177	M. pneumoniae 16S-
	94	19.8	4.5	26	1	AED69061	Kelp gametocyte rD
c	95	19.6	4.4	20	1	AAV34338	Burkholderia casid
c	96	19.6	4.4	20	1	AAX01434	Probe for Bacteroi
c	97	19.6	4.4	20	1	AAX59995	PCR primer 15R use
c	98	19.6	4.4	20	1	ABL59060	Nucleotide sequenc
c	99	19.6	4.4	20	1	ADM81035	Microbial 16SrDNA
c	100	19.6	4.4	20	1	AEA15813	Human Enterobacter
c	101	19.4	4.4	21	1	AAQ10128	Probe 1641 to the
c	102	19.4	4.4	21	1	AAQ10126	Probe 1639 to the
c	103	19.4	4.4	21	1	AAT11574	16S rRNA reverse p
c	104	19.4	4.4	21	1	AAT11572	16S rRNA reverse p
c	105	19.4	4.4	21	1	AAV21119	16S rRNA Escherich
c	106	19.4	4.4	21	1	AAV21121	16S rRNA Escherich
c	107	19.4	4.4	21	1	ADY97904	Bacillus subtilis
c	108	19.2	4.3	20	1	AAV61116	Lactobacillus sp.
c	109	19.2	4.3	20	1	AAV58223	Lactobacillus sp.
c	110	19.2	4.3	20	1	ADQ16363	PCR primer used to
c	111	19.2	4.3	20	1	AEA01079	Eubacterial 16S rD
	112	19.2	4.3	20	1	AEB93870	Mycoplasma PCR pri
c	113	19	4.3	19	1	AAZ91775	Spacer region betw
c	114	19	4.3	19	1	AAA92293	16S ribosomal DNA
c	115	19	4.3	19	1	AAF82059	16SrRNA PCR primer
c	116	19	4.3	19	1	AAF82062	16SrRNA PCR primer
c	117	19	4.3	19	1	AAI71859	Pectinatus frising
c	118	19	4.3	19	1	ABA04396	Fucophilus fucoida
c	119	19	4.3	19	1	ADF91902	16S ribosomal DNA
c	120	19	4.3	19	1	ADO42929	Primer of the inve
c	121	19	4.3	19	1	ADQ94518	Melanin inhibitor-
c	122	19	4.3	19	1	ADS19039	PCR primer used to
c	123	19	4.3	19	1	ADW11499	PCR primer used to
	124	19	4.3	19	1	ADW42907	Lactobacillus dete
	125	19	4.3	19	1	ADW42918	Lactobacillus dete
c	126	19	4.3	19	1	ADY71484	Geobacillus solubi
c	127	19	4.3	19	1	AEC08761	16s ribosomal DNA
	128	19	4.3	20	1	AAQ62086	Lactobacillus 16S/
	129	19	4.3	20	1	AAQ88220	Lactobacillus sp.
c	130	19	4.3	20	1	ADP47554	Intelligent PCR pr
c	131	19	4.3	20	1	ADQ59912	Intelligent PCR pr
c	132	19	4.3	20	1	AEC39825	D-hydantoinase enz

c	133	19	4.3	20	1	AED28920	Primer for PCR det
c	134	19	4.3	20	1	AEF81510	Halorubrum sp. BD-
c	135	19	4.3	20	1	AEE18738	Eubacteria univers
c	136	19	4.3	20	1	AEE94389	Universal bacteria
c	137	19	4.3	21	1	AAA74501	PCR primer ENV2B.
c	138	19	4.3	21	1	ABK14158	Chlorinated ethyle
c	139	19	4.3	21	1	ADN59207	Microorganism moni
c	140	19	4.3	21	1	ADN96852	Bacterial 16S rDNA
c	141	19	4.3	21	1	AEC07076	16S rRNA PCR prime
	142	19	4.3	23	1	AEA61056	Mycobacterium prob

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:28:49 ; Search time 0.001 Seconds
                                              (without alignments)
                                              675.376 Million cell updates/sec

Title: US-10-600-642A-2-COPY
Perfect score: 442
Sequence: 1 gaagtcgtaacaaggtagcc..........agcggttatggaaagtttaa 442

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 0.5

Searched: 33 seqs, 764 residues

Total number of hits satisfying chosen parameters: 66

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 33 summaries

Database :   pubnewdb2:*   score length PGPub new
                                                             8102
        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
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        2   25   5.7   25 1 US-11-348-413-988264   Sequence 988264,
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  c   4   22   5.0   28 1 US-11-255-290-7   Sequence 7, Appli
  c   5   21.6   4.9   22 1 US-11-265-833-2   Sequence 2, Appli
  c   6   21.2   4.8   27 1 US-11-368-333-6   Sequence 6, Appli
  c   7   20   4.5   20 1 US-10-510-329-13   Sequence 13, Appl
  c   8   20   4.5   20 1 US-11-324-675-2   Sequence 2, Appli
  c   9   19   4.3   19 1 US-11-373-989-2   Sequence 2, Appli
       10   18.8   4.3   25 1 US-11-348-413-1009479   Sequence 1009479,
       11   18.6   4.2   25 1 US-11-348-413-1064914   Sequence 1064914,
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       16   18.2   4.1   25 1 US-11-348-413-1055941   Sequence 1055941,
  c   17   18   4.1   18 1 US-11-350-955-9   Sequence 9, Appli
  c   18   18   4.1   18 1 US-11-350-796-9   Sequence 9, Appli

c	19	17.8	4.0	25	1	US-11-348-413-1009551	Sequence 1009551,
c	20	17.6	4.0	25	1	US-11-348-413-222739	Sequence 222739,
	21	17.6	4.0	25	1	US-11-348-413-434686	Sequence 434686,
	22	17.6	4.0	25	1	US-11-348-413-434687	Sequence 434687,
	23	17.6	4.0	25	1	US-11-348-413-572608	Sequence 572608,
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	25	17.6	4.0	25	1	US-11-348-413-930121	Sequence 930121,
	26	17.6	4.0	25	1	US-11-348-413-1075989	Sequence 1075989,
	27	17.6	4.0	25	1	US-11-348-413-1238534	Sequence 1238534,
c	28	17.4	3.9	19	1	US-10-034-622-2	Sequence 2, Appli
c	29	17.4	3.9	19	1	US-11-134-852-2	Sequence 2, Appli
c	30	17.4	3.9	19	1	US-11-235-479-5	Sequence 5, Appli
c	31	17	3.8	17	1	US-10-524-152A-12	Sequence 12, Appl
c	32	17	3.8	18	1	US-10-524-152A-10	Sequence 10, Appl
	33	16.4	3.7	22	1	US-10-535-629-9	Sequence 9, Appli